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GAATTCGGAC GAATTATTC AATCATAAAC ACAAATAAAC ATTTCAGTAG TTCCCCACCA	60
CACACACACA CACAGCCCCG GCAITATTAC ACTAAALACG ACACATCAATC CAAAMALTC	120
GCACCAAAA CATCAATAAA C ATC CAT TCC ATT AAA TGT TTA TTA ACA GCA	171
Met His Trp Ile Lys Cys Leu Leu Thr Ala	10
TTC ATT TCC TTC ACA GTC ATC GTC CAC GTT CAC AGT TCC GCC ACC TTT	219
Phe Ile Cys Phe Thr Val Ile Val Glu Val His Ser Ser Gly Ser Phe	25
CAC TTG CCC CTC AAC TAC TTC ACC AAC CAT CAC CCC CGG CAC AAC CAC	267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asn His Gly Arg Asn Asn Glu	40
CGT CGC TCC TCC ACC GCG CAC TCC CAC GGA CCG ACC CCC AAC TCC CTC	315
Gly Arg Cys Cys Ser Gly Glu Ser Asn Gly Ala Thr Gly Lys Cys Leu	55
CGC ACC TCC AAC ACC CCG TTT CCG CTC TCC CTA AAC CAC TAC CAC GCC	363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Glu Ala	70
AAC ATC CAC ACC ACC TCC CAC TCC ACC TAC GCG CAC CTC ATC ACC CCC	411
Thr Ile Asn Thr Thr Ser Glu Cys Thr Tyr Gly Asn Val Ile Thr Pro	90
ATT CTC GCG CAC AAC TCC CTC AAT CTC ACC CAC CCC CAC CCC TTC CAC	459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asn Ala Glu Arg Phe Glu	105
AAC AAC CCG TTC ACC AAT CCC ATC CAC TTC CCC TTC TCC TTC TCA TCG	507
Asn Lys Gly Phe Thr Asn Pro Ile Glu Phe Pro Phe Ser Phe Ser Trp	120
CCG GGT ACC TTC TCC CTC ATC CTC CAC CCC TCC CAT CAT ACC AAC AAT	555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asn Thr Asn Asn	135
ACC CGC AAT CCG CGA ACC AAC AAC CTC CTC ATC CAC CGA CTC TTC GTG	603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Glu Arg Leu Leu Val	150
CAC CAC GTA CTC CAC CTC TCC TCC CAA TCC AAC ACC AAC AAC TCC CAA	651
Glu Glu Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu	170
TCC CAC TAC ACC TCC CTC CAC TAC CAT TTC CGT CTC ACC TCC CAT CTC	699
Ser Glu Tyr Thr Ser Leu Glu Tyr Asn Phe Arg Val Thr Cys Asn Leu	185
AAC TAC TAC GGA TCC GCG TGT CCC AAC TTC TCC CCG CCC CCG CAC CAT	747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asn Asn	200
TCA TTT CCA CAC TCC ACT TCC TCC CAC ACC GCG CAA ATT ATC TGT TTC	795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu	215
ACC CGA TCC CAC GCG CAT TAC TGT CAC ATA CCC AAA TCC GCG AAA GCG	843
Thr Gly Trp Glu Gly Asn Tyr Cys His Ile Pro Lys Cys Ala Lys Gly	230
TGT CAA CAT CCA CAT TCC CAC AAA CCC AAT CAA TCC GTT TCC CAA CTC	891
Cys Glu His Gly His Cys Asn Lys Pro Asn Glu Cys Val Cys Glu Leu	250

Figure 1 Cont'D

CCC TCC AAC CCA CCC TTC TCC AAC CAC TCC GTT CTC GAA CCG AAC TCC Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys 255 260 265	939
ATC CAT CCC ACC TCC AAC AAA CCC TCC ACT TCC ATC TCC AAC CAC CCT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TGG GCA CCC TTC TAC TCC AAC CAC CAT CTC AAC TAC TCC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Glu Asn Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
AGA CCC TCC AAC AAT GGC GCA ACC TCC TTC AAC ACC GGC CAC GCA TTC Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TCC AAA TCC CCT CCA GCA TAC AGT CGT CAT CAT TCC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asn Asn Cys Glu Asn 315 320 330	1131
CAC ATC TAC TCC TCC GAT CCC GAT GTC AAT CCC TCC CAC AAT CCT CCT Glu Ile Tyr Ser Cys Asn Ala Asn Val Asn Pro Cys Glu Asn Gly Gly 335 340 345	1179
ACC TCC ATC GAT CAC CCC CAC ACA AAA ACC GGC TAC AAC TGT CAT TCC Thr Cys Ile Asn Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
CCC AAC CCC TCC ACC GCA AAC ATC TCC CAC CAC AAA CTC CTC ACC TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TCC CAC AAA CCC TGT CAT CAC GCA ATC TCC CCC AAC GTT CCT CCT GGC Ser Asn Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 390	1323
TTC GCA ACC AAC CCT CAC GGC TAC CAC TCC GAA TGT CCC ATT CCC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371
ACC GCA CCC AAC TCC CAT CTC CAC CTC CAC AAC TCC AGT CCC AAT CCA Ser Gly Pro Asn Cys Asn Leu Gln Leu Asn Asn Cys Ser Pro Asn Pro 415 420 425	1419
TCC ATA AAC GGT GCA ACC TGT CAC CCC ACC GCA AAC TGT ATT TCC CCA Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro 430 435 440	1467
CCG GCA TTT TCC GCA ACC ACA TCC CAC ACC AAC ATT CAC CAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asn Asn Cys Leu 445 450 455	1515
CCC CAC CAC TCC CAC AAC GCA CCC ACC TCC ATA CAT ATC GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asn Met Val Asn Gln 460 465 470	1563
TAT CCC TCC CAA TCC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT ACC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser 475 480 485 490	1611
AAA GTT CAC TTC TCC CTC ATC ACA CCC TGT CCC AAT CCA GCA ACC TCC Lys Val Asn Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys 495 500 505	1659
TTC AAT CTC AAC AAC CAT TAC CAC TCC ACC TGT CCT CCC GCA TTT ACT Leu Asn Leu Asn Asn Asn Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr 510 515 520	1707

Figure 1 Cont'D

GGG	AAG	GAT	TCC	TCT	GTC	GAC	ATC	GAT	GAG	TCC	ACC	AGT	CGA	CCC	TGT	1755
Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
		525					530					535				
CAT	AAC	GGC	GCC	ACT	TCC	ATG	AAC	CGC	GTC	AAT	TCC	TTC	GAA	TCC	GTC	1803
His	Asn	Gly	Gly	Thr	Cys	Met	Asn	Arg	Val	Asn	Ser	Phe	Glu	Cys	Val	
		540				545					550					
TGT	CCC	AAT	GGT	TTC	ACG	GCC	AAC	CAG	TCC	GAT	CAG	GAG	TCC	TAC	GAT	1851
Cys	Ala	Asn	Gly	Phe	Arg	Gly	Lys	Gln	Cys	Asp	Glu	Glu	Ser	Tyr	Asp	
		555			560					565					570	
TCC	GTC	ACC	TTC	GAT	GCC	CAC	CAA	TAT	CCA	CCG	ACC	ACA	CAA	CCG	ACA	1899
Ser	Val	Thr	Phe	Asp	Ala	His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	
				575					580					585		
CCC	GAT	GGT	TTC	ACC	AAT	GCC	CAG	GTA	GTC	CTA	ATT	GCT	GTT	TTC	TCC	1947
Ala	Asp	Gly	Leu	Thr	Asn	Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	
			590					595					600			
GTT	CCC	ATC	CCT	TTC	GTC	GCC	GTT	ATT	CCG	CCG	TCC	GTC	GTC	TTC	TCC	1995
Val	Ala	Met	Pro	Leu	Val	Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	
		605					610					615				
ATG	AAC	CGC	AAC	CGT	AAC	CGT	CGT	CAG	CAA	AAC	CAC	CAC	CCC	CAC	CCC	2043
Met	Lys	Arg	Lys	Arg	Lys	Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	
		620				625					630					
ACG	AAC	CAG	AAC	CAA	CAG	AAT	GCC	GTC	CCC	ACA	ATC	CAT	CAC	AAT	GCC	2091
Arg	Lys	Gln	Asn	Glu	Gln	Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	
		635			640					645					650	
AGT	CGC	GTC	GGT	GTA	GCT	TTC	GCT	TCA	CCC	TCT	CTC	GGC	GGC	AAA	ACT	2139
Ser	Gly	Val	Gly	Val	Ala	Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	
				655					660					665		
CCC	ACC	AAC	ACC	GGT	CTC	ACC	TTC	GAT	GGC	GGC	AAC	CCG	AAT	ATC	ATC	2187
Gly	Ser	Asn	Ser	Gly	Leu	Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	
			670					675					680			
AAA	AAC	ACC	TCC	GAC	AAC	TCC	GTC	AAC	AAC	ATT	TGT	CCC	TCA	CCA	CCA	2235
Lys	Asn	Thr	Trp	Asp	Lys	Ser	Val	Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	
		685					690					695				
CCA	CCG	CCG	CCG	CCG	GCA	GCA	CCG	CCG	CAC	GAC	TGT	CTC	ATG	TAC	GGC	2283
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Glu	Cys	Leu-Met	Tyr	Gly		
		700				705					710					
CGA	TAT	GTC	CCC	TCC	GTC	CCG	GAT	AAC	AAC	AAT	CCC	AAC	TCA	GAC	TTC	2331
Gly	Tyr	Val	Ala	Ser	Val	Ala	Asp	Asn	Asn	Asn	Ala	Asn	Ser	Asp	Phe	
		715			720					725					730	
TGT	GTC	GCT	CCG	CTA	CAA	ACA	GCC	AAC	TCC	CAA	AAC	CAA	CTC	AAC	ACC	2379
Cys	Val	Ala	Pro	Leu	Gln	Arg	Ala	Lys	Ser	Gln	Lys	Gln	Leu	Asn	Thr	
			735					740					745			
GAT	CCC	ACC	CTC	ATG	CAC	CCG	GGT	TCC	CCG	GCA	GGC	ACC	TCA	GCC	AAC	2427
Asp	Pro	Thr	Leu	Met	His	Arg	Gly	Ser	Pro	Ala	Gly	Ser	Ser	Ala	Lys	
			750					755					760			
CGA	CCG	TCT	CCC	CGA	CGA	CCG	CGA	CCC	CCC	CAC	GGC	AAC	ACC	ATC	TCT	2475
Gly	Ala	Ser	Gly	Gly	Gly	Pro	Gly	Ala	Ala	Glu	Gly	Lys	Arg	Ile	Ser	
		765					770					775				
GTT	TTA	GCC	CAC	GCT	TCC	TAC	TGT	ACC	CAC	CGT	TCC	CCC	TCC	TTC	CCC	2523
Val	Leu	Gly	Glu	Gly	Ser	Tyr	Cys	Ser	Gln	Arg	Trp	Pro	Ser	Leu	Ala	
		780				785					790					

Figure 1 Cont'D

CCC CCG CCA CTC CCC CCA CCC TGT TCA TCC CAG CTA ATC GCT CCA CCT	2571
Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Glu Leu Met Ala Ala Ala	
795 000 005 010	
TCG CCA CCG GCG ACC CCA CCG CCG ACC GCG CAA CAG CAG CCA TCC CTC	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Glu Glu Glu Arg Ser Val	
015 020 025	
CTC TCC GCG ACT CCC CAT ATG TAACTCCAAA AATCCCGAAG CCGTCCCTCT	2670
Val Cys Gly Thr Pro His Met	
030	
AAATCCGGAG AAATCCGGAT GCAAGAGCTC ACAGCAGATA CACAAAGAAA AGACTGGGTT	2730
CGGTTCAGAA TGTGAGAGAG AGCCCAAAAT GTTGTTCCTT ATTCAGGCAG TTTAGTCGTC	2790
ACGAAAAATC AAAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAAATTACCA AGCTGTGACC CAGCCGTTTC CATCCCGAAT TC	2892

Figure 2

		% Aggregation with DI with Ser	
1. pMINMg		40	21
2. ΔSph		0	nl
3. ΔC1a		0	nl
4. ΔEGF(7-17)		0	nl
5. ΔEGF(9-26)		0	nl
6. ΔEGF(17-30)		22	nl
7. ΔEGF(7-9)		20	14
8. ΔEGF(9-17)		0	0
9. ΔEGF(17-26)		10	8
10. ΔEGF(26-30)		5	7
11. ΔEGF(9-30)		0	nl
12. ΔEGF(7-26)		0	nl
13. ΔC1a+EGF(9-17)		35	20
14. ΔC1a+EGF(17-26)		0	nl
15. split		42	nl
16. ΔC1a+EGF(9-13)		47	25
17. ΔC1a+EGF(11-15)		0	0
18. ΔC1a+EGF(13-17)		0	nl
19. ΔC1a+EGF(10-13)		56	23
20. ΔC1a+EGF(11-13)		0	nl
21. ΔC1a+EGF(10-12)		0	nl
22. ΔC1a+EGF(10-11)		0	nl
23. ΔC1a+EGF(10-12)		45	nl
24. ΔC1a+EGF(11-12)		11	nl
25. ΔEGF		0	nl
26. ΔEGF+EGF(9-17)		24	nl
27. ΔEGF+EGF(9-13)		40	nl
28. ΔEGF+EGF(10-13)		45	23
29. ΔEGF+EGF(10-12)		48	nl
30. ΔECN		0	nl
31. ΔECN+EGF(10-13)		26	nl
32. ΔECN+EGF(10-12)		47	22
33. ΔC1a+ΔEGF(10-13)		42	20

Figure 3

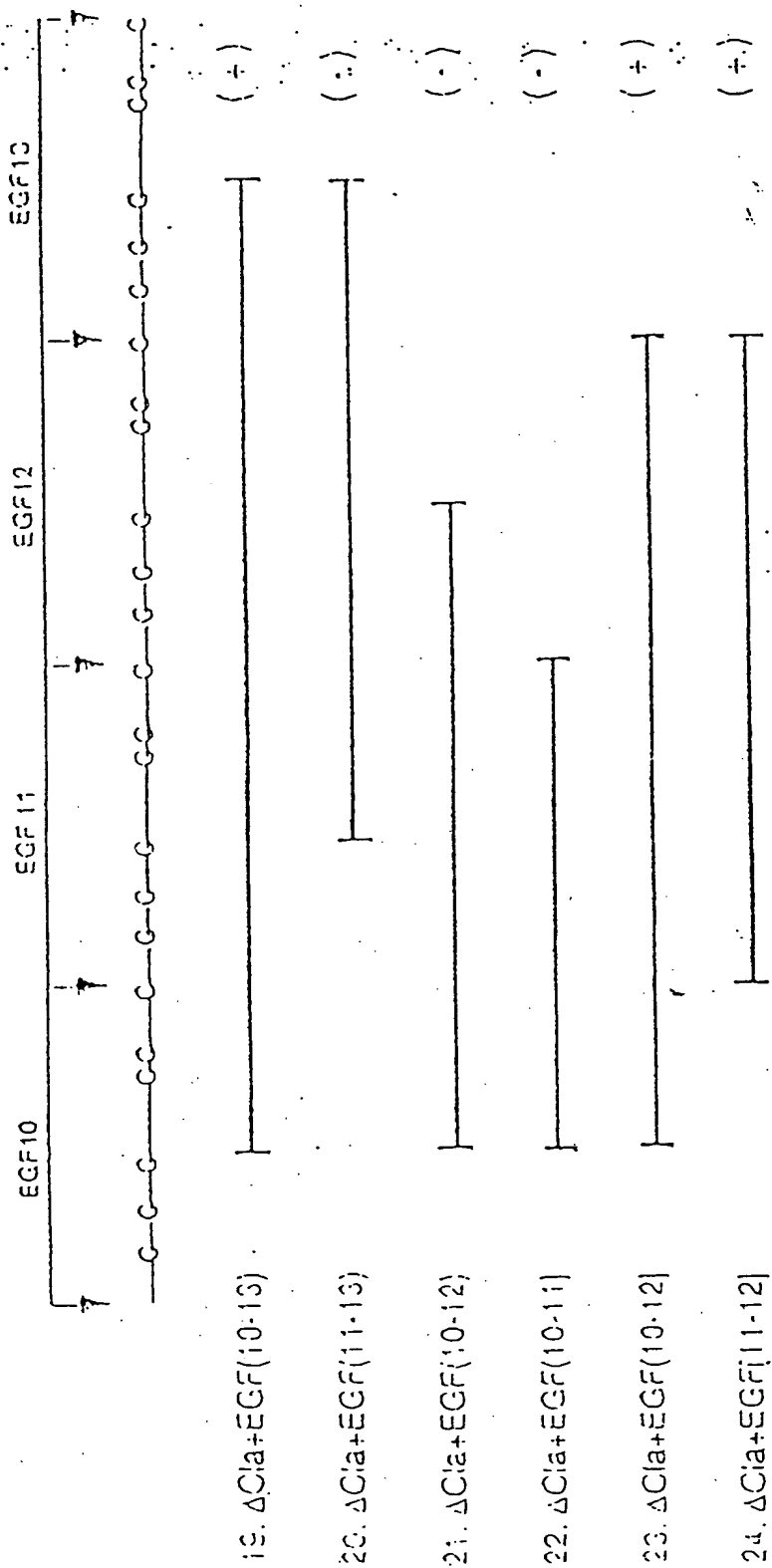
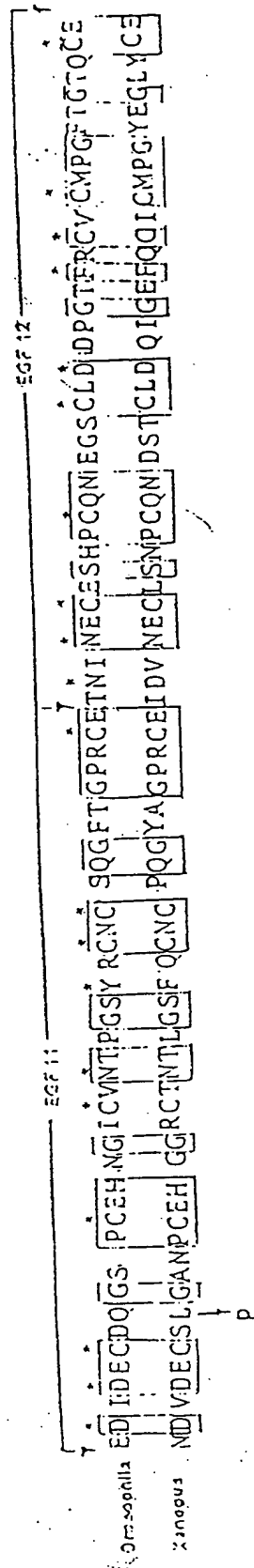


Figure 4



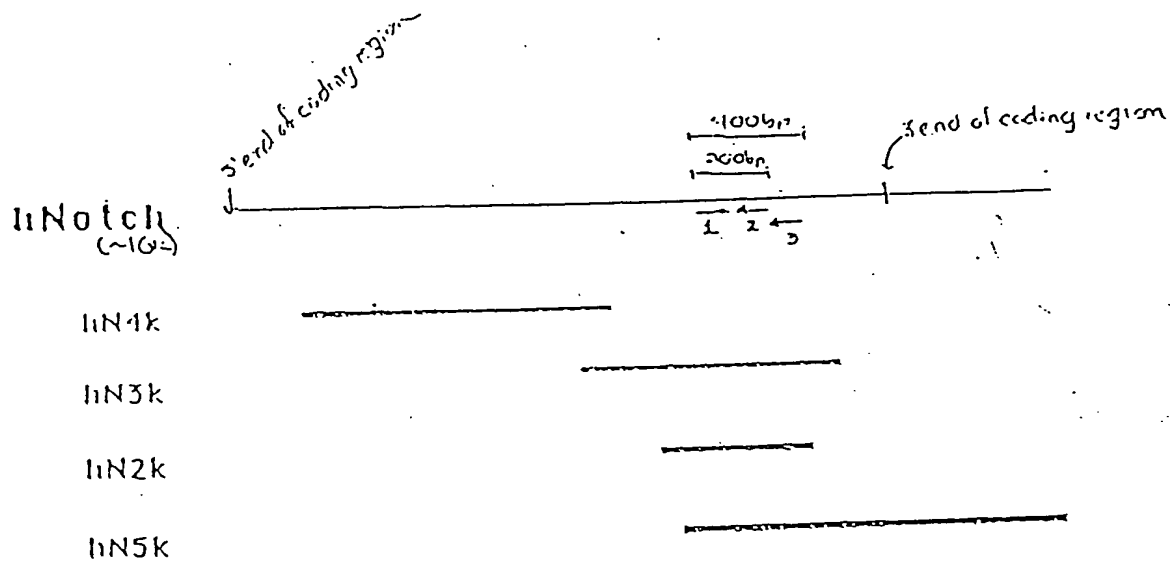


Figure 6

Figure 7

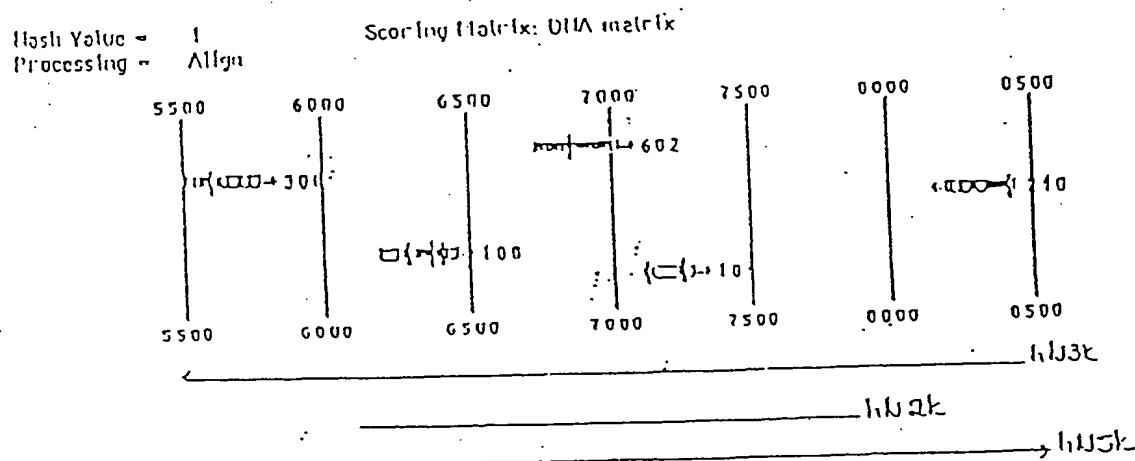
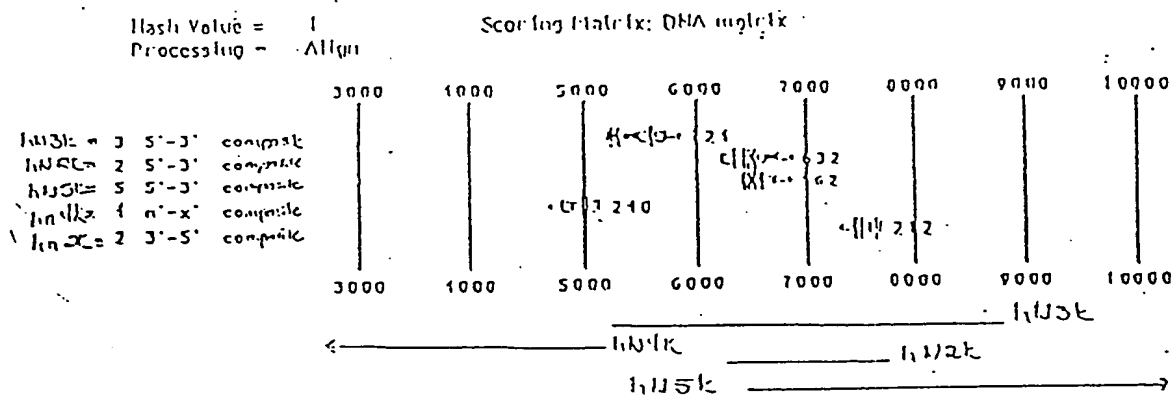


Figure 8A

A.

```

1  GAAATCCGCT GGGAGGAAATGG TCTGAGCTAC CTGCCCCGTCC TGCTGGGGCA TCANTGGCAH
61  GTGGGGGAAAG CCRCACTGGG CAAACGGGCC AGGCCAATTC TCGAATGTGG TACATCGTGG
121  GCAGGGGGGCC CGCAGCAGCT GCGAGGCGAGG TGGACTGAGG CTGGGGATCC CCGCTGCTT
181  GGGCAATAGT GCGTTTACCC ATGAGCTGGH AAGTCACAAI GGGGGGCAAG GGTCCCGAG
241  GGIGGTATG TGCTTCCTTC AGGTGGC

```

Figure 8B

B.

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1  GAAATCCCTC CATIATACGT GACTTTTCTG AARCTGAGC CACCCTAGTG TCCTTAACTC
61  CCTCTGGAGT TTGTAGCTT TGGTCTTTC AAGAGCGAGG CTCTCTTCAH GCTCCTTAAT
121  GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACTT TTGGTAATIG ATTCTTCTTC
181  AACCCCGAAC TCAAGGCTGG CTCTCACTCT CTAGGCAAGG CAGGAAITCC GAGGTGGATG
241  TGTTAGATGT GAATGTCCGT GGGCCAGATG GCTGCACCCC ATIGATGTIG GCTTCTCTCC
301  GAGGAGGCCAG CTCAGATTTG AGTCATCAAG ATCAAGATCC AGAGCACTCT TCTGCTAACA
361  TCATCACAGA CTGGGTCTAC CAGGGTGCCA GCTCCAGHC CAGACAGACC GGACTGGTGA
421  GATGGCCCTG CACCTTGCAG CCGCTTACTC AGGGGCTGAT GCTGCCAAGC GTCTCTCTGA
481  TGCAGGTGCA GATGCCAATG CCGAGGACAA CATGGGCCCG TGTCACITCC ATGCTGCAGT
541  GGCACGTGAT GCCAGGTCT ATTCAAGTCT GTTA

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Figure 8C

C.

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1  TCCAGATICT GATTCGCAC CAGCTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA
61  CACCCCTGAT CCTGGCTGCC CCGCTGGCTG TCGACCGAAT GGTGCCAGAA CTGATCAACT
121  GCGAGCGGGA TGTGAATGCA GTGGATGACC ATCGAATAIC TCTCTTCAC TGGGCAGCTG
181  CTGTCAATTA TGTGGAGGCA ACCTTTTGT TGTGAAAAA TCGGGCCAC CAGACATGC
241  AGCAGACAAA GCAAGAGACA CCTCTGTTC TTGCTGCCCG GGAGCAGCTA TAGG

```

Figure 9A

```

1  GAATTCATTT CAGGAGGAAA GGGTGGGGAG ACNAGCAGGC ACCCACTTTC CCGTGGGTGG
61 ACTCGTTCCC AGGTGGGTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CCGAGTGCCA
121 TTCAGAAAT TCCAGAAAG CCGTACCCCA ACTCGGACGG CAGAGTCACA CCCCTGGGTA
181 GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGACGGG GGGATGGCAC CCCCTGCAGG
211 CAGAGCTG

```

Figure 9B

```

1  CTAAAGGGAA CAAAGGCHGG AGCTCCACCC CGGGCGGCHC HGCTCTAGAA CTAGTGGANH
61 HCCCGGGCTG CAGGAATTC GGGGGACTGG GCTCGGGCTC AGAGCGGGCG TGTGAGAG
121 ATTCTAGACC GGGAGAGCAA GCGRATGGCT GACAGCTGGC CTCCAAAGTC ACCAGGCTCA
181 ATTCGCTCGC CCGGACATC GAGCGATGCA GAGGATCAGA ACCGGTACCT GGTGGGATG
241 ACTCGGATTT ACAAGCATGA CAGGCTGTCT TACAGGGAGC GTGAHHITTT CACATGCAGT
301 CGACAGACAC GAGCTCTATG CAT

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Figure 10

7326-131

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      10      20      30      40
TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC
C   Q   E   D   A   G   N   K   V   C   S   L   Q   C   N   N>

50      60      70      80      90
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC
H   A   C   G   W   D   G   G   D   C   S   L   N   F   N   D>

100     110     120     130     140
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT
P   W   K   N   C   T   Q   S   L   Q   C   W   K   Y   F   S>

150     160     170     180     190
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC
D   G   H   C   D   S   Q   C   N   S   A   G   C   L   F   D>

200     210     220     230     240
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC
G   F   D   C   Q   R   A   E   G   Q   C   N   P   L   Y   D>

250     260     270     280
CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC
Q   Y   C   K   D   H   F   S   D   G   H   C   D   Q   G   C>

290     300     310     320     330
AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG CAC TGT GCG GAG CAT GTA
N   S   A   E   C   E   W   D   G   L   D   C   A   E   H   V>

340     350     360     370     380
CCC GAG AGG CTG GCG GCC GGC ACG CTG GTG GTG GTG GTG CTG ATG CCG
P   E   R   L   A   A   G   T   L   V   V   V   V   L   M   P>

390     400     410     420     430
CCG GAG CAG CTG CGC AAC AGC TCC TTC CAC TTC CTG CGG GAG CTC AGC
P   E   Q   L   R   N   S   S   F   H   F   L   R   E   L   S>

440     450     460     470     480
CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG
R   V   L   H   T   N   V   V   F   K   R   D   A   H   G   O>

490     500     510     520
CAG ATG ATC TTC CCC TAC TAC GGC CGC GAG GAG GAG CTG CGC AAG CAC
Q   M   I   F   P   Y   Y   G   R   E   E   E   L   R   K   H>

530     540     550     560     570
CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG
P   I   K   R   A   A   E   G   W   A   A   P   D   A   L   I>

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```

      580      590      600      610      620
    GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG
      G   Q   V   K   A   S   L   L   P   G   G   S   E   G   G   R>

      630      640      650      660      670
    CGG GGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
      R   R   R   E   L   D   P   M   D   V   R   G   S   I   V   Y>

      680      690      700      710      720
    CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
      L   E   I   D   N   R   Q   C   V   Q   A   S   S   Q   C   F>

      730      740      750      760
    CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG
      Q   S   A   T   D   V   A   A   F   L   G   A   L   A   S   L>

      770      780      790      800      810
    GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GCC GTG CAG AGT GAG ACC
      G   S   L   N   I   P   Y   K   I   E   A   V   Q   S   E   T>

      820      830      840      850      860
    GTG GAG CCG CCC CCG CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG
      V   E   P   P   P   P   A   Q   L   H   F   M   Y   V   A   A>

      870      880      890      900      910
    GCC GCC TTT GTG CTT CTG TTC TTC GTG GGC TGC GGG GTG CTG CTG TCC
      A   A   F   V   L   L   F   F   V   G   C   G   V   L   L   S>

      920      930      940      950      960
    CGC AAG CGC CGG CGG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC
      R   K   R   R   R   Q   H   G   Q   L   W   F   P   E   G   F>

      970      980      990      1000
    AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG
      K   V   S   E   A   S   K   K   K   R   R   E   P   L   G   E>

      1010      1020      1030      1040      1050
    GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC
      D   S   V   G   L   K   P   L   K   N   A   S   D   G   A   L>

      1060      1070      1080      1090      1100
    ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG
      M   D   D   N   Q   N   E   W   G   D   E   D   L   E   T   K>

      1110      1120      1130      1140      1150
    AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG
      K   F   R   F   E   E   P   V   V   L   P   D   L   D   D   Q>

      1160      1170      1180      1190      1200

```

ACA GAC CAC CGG CAG TGG ACT CAG CAG CAC CTG GAT GCC GCT GAC CTG
 T D H R Q W T Q Q H L D A A D L>

1210 1220 1230 1240
 CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC
 R M S A M A P T P P Q G E V D A>

1250 1260 1270 1280 1290
 GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC
 D C M D V N V R G P D G F T P L>

1300 1310 1320 1330 1340
 ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG
 M I A S C S G G G L E T G N S E>

1350 1360 1370 1380 1390
 GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC
 E E E D A P A V I S D F I Y Q G>

1400 1410 1420 1430 1440
 GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC
 A S L H N Q T D R T G E T A L H>

1450 1460 1470 1480
 CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG
 L A A R Y S R S D A A K R L L E>

1490 1500 1510 1520 1530
 GCC AGC GCA GAT GCC AAC ATC CAG GAG AAC ATG GGC CGC ACC CCG CTG
 A S A D A N I Q D N M G R T P L>

1540 1550 1560 1570 1580
 CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC
 H A A V S A D A Q G V F Q I L I>

1590 1600 1610 1620 1630
 CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG
 R N R A T D L D A R M H D G T T>

1640 1650 1660 1670 1680
 CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC
 P L I L A A R L A V E G M L E D>

1690 1700 1710 1720
 CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG
 L I N S H A D V N A V D D L G E>

1730 1740 1750 1760 1770
 TCC GCC CTG CAC TGG GCC GCC GCC GTG AAC AAT GTG GAT GCC GCA GTT
 S A L H W A A A V H H V D A A V>

1780	1790	1800	1810	1820
GTG CTC CTG MAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG				
V L L K N G A N K D M Q N N R E>				
1830	1840	1850	1860	1870
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCG				
E T P L F L A A R E G S Y E T A>				
1880	1890	1900	1910	1920
MAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG				
K V L L D H F A N R D I T D H M>				
1930	1940	1950	1960	
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC				
D R L P R D I A Q E R M H H D I>				
1970	1980	1990	2000	2010
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC				
V R L L D E Y N L V R S P Q L H>				
2020	2030	2040	2050	2060
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG				
G A P L G G T P T L S P P L C S>				
2070	2080	2090	2100	2110
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG				
P N G Y L G S L K P G V Q G K K O>				
2120	2130	2140	2150	2160
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC				
V R K P S S K G L A C G S K E A>				
2170	2180	2190	2200	
AAG GAC CTC AAG GCA CGG AAG AAG AAG TCC CAG GAT GGC AAG GGC TGC				
K D L K A R R K K S Q D G K G C>				
2210	2220	2230	2240	2250
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA				
L L D S S G H L S P V D S L E S>				
2260	2270	2280	2290	2300
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC				
P H G Y L S D V A S P P L L P S>				
2310	2320	2330	2340	2350
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG				
P F Q Q S P S V P L H H L P G M>				
2360	2370	2380	2390	2400

Figure 10 Cont'D

CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC
 P D T H L G I G H L N V A A K P>

2410 2420 2430 2440
 CAG ATG GCG GCG CTG GGT GGG GGC GGC CGG CTG GCC TTT GAG ACT GGC
 E M A A L G G G G R L A F E T G>

2450 2460 2470 2480 2490
 CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC
 P P R L S H L P V A S G T S T V>

2500 2510 2520 2530 2540
 CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC
 L G S S S G G A L N F T V G G S>

2550 2560 2570 2580 2590
 ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC
 T S L N G Q C E W L S R L Q S G>

2600 2610 2620 2630 2640
 ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC
 M V P N Q Y N P L R G S V A P G>

2650 2660 2670 2680
 CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG
 P L S T Q A P S L Q H G M V G P>

2690 2700 2710 2720 2730
 CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC
 L H S S L A A S A L S Q M M S Y>

2740 2750 2760 2770 2780
 CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG
 Q G L P S T R L A T Q P H L V Q>

2790 2800 2810 2820 2830
 ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG
 T Q Q V Q P Q N L Q M Q Q Q N L>

2840 2850 2860 2870 2880
 CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA
 Q P A H I Q Q Q Q S L Q P P P P>

2890 2900 2910 2920
 CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG
 P P Q P H L G V S S A A S G H I>

2930 2940 2950 2960 2970
 GGC CGG AGC TTC CTG AGT GCA GAG CCG AGC CAG GCA GAC GTG CAG CCA

Figure 10 Cont'D

G R S F L S G E P S Q A D V Q P>
 2980 2990 3000 3010 3020
 CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC
 L G P S S L A V H T I L P Q E S>
 3030 3040 3050 3060 3070
 CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC
 P A L P T S L P S S L V P P V T>
 3080 3090 3100 3110 3120
 GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT
 A A Q F L T P P S Q H S Y S S P>
 3130 3140 3150 3160
 GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG
 V D N T P S H Q I Q V P V P V M>
 3170 3180 3190 3200 3210
 GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC
 V M I R S S D P S K G S S I L I>
 3220 3230
 GAA GCT CCC GAC TCA TGG
 E A P D S W>

G GAG GTG GAT GTG TTA GAT GTG AAT GTG CCG CCC CCA GAT GCG TCG Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Phe Asp Gly Cys 1 5 10 15	46
ACC CCA TTC ATG TGC GGT TGT CTC CCA CCA GCG AGC TCA GAT TTC ACT Thr Phe Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 30	94
GAT GAA GAT GAA GAT CCA GAG GAC TCT TCT CCG AAC ATC ATC ACA GAG Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTC GTG TAC GAG GGT CCC AAC CTC GAG CCC CAG ACA GAG CCG ACT GGT Leu Val Tyr Glu Gly Ala Ser Leu Glu Ala Glu Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG CCC CTC GAG CTT CCA CCC CCG TAC TCA CCG GGT GAT GGT CCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	230
AAC CGT CTC CTC GAT CCA GGT CCA GAT CCG AAT CCC CAG GAG AAC ATC Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Glu Asp Asn Met 80 85 90 95	286
GGC CCC TGT CCA CTC GAT GGT CCA GTG CCA GGT GAT GCG CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Glu Gly Val 100 105 110	334
TTC CAG ATT CTC ATT CCC AAC CGA GTA ACT GAT GTA GAT CCC AGG ATC Phe Glu Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT CCG ACT ACA CCC CTC ATC CTC GGT GCG CCC CTC GGT GTC GAG Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430
CCA ATC GTC CCA GAA CTC ATC AAC TGC CAA CCG GAT GTC AAT CCA GTC Gly Met Val Ala Glu Leu Ile Asn Cys Glu Ala Asp Val Asn Ala Val 145 150 155	478
GAT GAG CAT CCA AAA TCT GGT CTT GAG TGG CCA GGT GGT GTC AAT AAT Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Val Asn Asn 160 165 170 175	526
CTG GAG CCA ACT CTT TTG TTG TTG AAA AAT GCG CCC AAC CCA GAG ATC Val Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met 180 185 190	574
CAG GAG AAC AAC CAA GAG ACA CCG CTC TTT CTT CCG CCC CAG GCG Glu Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly 195 200 205	622
AGC TAT CAA CCA CCC AAC ATC CTC TTA GAG CAT TTT CCC AAT CCA GAG Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp 210 215 220	670
ATC ACA GAG CAT ATC GAT CCG CTT CCC CCG CAT GTC CCG CCG CAT CCC Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg 225 230 235	718
ATC CAG CAT GAG ATT CTC CCC CTT CTC GAT CAA TAC AAT GTC ACC CCA Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro 240 245 250 255	766

Figure 11 Cont'D

AGC	CCT	CCA	GGC	ACC	GTC	TTG	ACT	TCT	GCT	CTC	TCA	CCT	GTC	ATC	TGT	014
Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Val	Ile	Cys	
				260					265					270		
CCC	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CIG	AAG	CAC	ACC	CCA	ATC	CCC	AAG	062
Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His	Thr	Pro	Met	Gly	Lys	
			275					280					285			
AAG	TCT	AGA	CCC	CCC	AGT	CCC	AAC	AGT	ACC	ATC	CCT	ACT	ACC	CTC	CCT	310
Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met	Pro	Thr	Ser	Leu	Pro	
			290				295					300				
AAC	CTT	CCC	AAG	CAC	GCA	AAG	GAT	CCC	AAG	CCT	AGT	AGC	AGC	AAG	AAG	950
Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly	Ser	Arg	Arg	Lys	Lys	
			305			310					315					
TCT	CTC	AGT	CAC	AAG	GTC	CAA	CTC	TCT	CAC	AGT	TCA	GTA	ACT	TTA	TCC	1006
Ser	Leu	Ser	Glu	Lys	Val	Glu	Leu	Ser	Glu	Ser	Ser	Val	Thr	Leu	Ser	
					325					330					335	
CCT	GTT	GAT	TCC	CTA	CAA	TCT	CCT	CAC	ACC	TAT	GTT	TCC	CAC	ACC	ACA	1054
Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr	Val	Ser	Asp	Thr	Thr	
				340					345					350		
TCC	TCT	CCA	ATC	ATT	ACA	TCC	CCT	GGG	ATC	TTA	CAG	CCC	TCA	CCC	AAC	1102
Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu	Glu	Ala	Ser	Pro	Asn	
				355				360					365			
CCT	ATC	TTC	CCC	AGT	CCC	CCC	CCT	CCT	CCC	CCA	CTC	CAT	CCC	CAG	CAT	1150
Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Glu	His	
				370			375					380				
CCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	ATC	CAG	CCT	TTC	CCA	CAT	CCG	1198
Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Glu	Pro	Leu	Ala	His	Gly	
						390					395					
CCC	ACC	ACT	GTC	CTT	CCC	TCA	GTC	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Glu	Leu	Leu	Ser	His	His	His	
					405				410						415	
ATT	GTC	TCT	CCA	GGC	AGT	GGC	AGT	CCT	GCA	ACC	TTC	AGT	ACC	CTC	CAT	1294
Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	
				420				425						430		
CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATC	AAC	CCC	ATC	CAG	GTC	AAT	CAC	1342
Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	
				435				440					445			
ACC	CAC	TAC	AAT	CAG	ATC	TTT	GCT	ATC	GTC	CTC	CCT	CCA	CCT	CAC	CCC	1390
Thr	Glu	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	
				450			455					460				
ACC	CAT	CCT	CCC	ATA	CCT	CCC	CAG	AGC	AGC	CCA	CCT	GAA	CCC	AAG	CAC	1430
Thr	His	Pro	Gly	Ile	Ala	Pro	Glu	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	
				465		470				475						
ATA	ACC	ACC	CCT	CCG	CAC	CCC	TTC	CCC	CCC	ATT	GTC	ACT	TTC	CAG	CTC	1486
Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Glu	Leu	
				485				490							495	
ATC	CCT	AAA	CCC	AGT	ATT	CCC	CAA	CCA	CCC	CCC	CCT	CCC	CAG	CCT	CAC	1534
Ile	Pro	Lys	Gly	Ser	Ile	Ala	Glu	Pro	Ala	Gly	Ala	Pro	Glu	Pro	Glu	
				500				505						510		
TCC	ACC	TCC	CCT	CCA	CCT	GTT	GGC	GGC	CCC	CTC	CCC	ACC	ATC	TAC	CAC	1582
Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Glu	
				515				520					525			
ATT	CCA	CAA	ATC	CCG	CCT	TTC	CCC	AGT	GTC	CCT	TTC	CCC	ACT	CCC	ATC	1630
Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	
				530			535						540			

Figure 11 Cont'D

ATC CCC CAG CAG CAG GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT TTC CCA GCC TCT CTC GCG AAC TAC CCC ACA CCG CCT TCA CAG His Pro Phe Phe Ala Ser Val Gly Tyr Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT GGT TCC TCA AAT GCT GCT GAG CGA ACA CCG AGT CAC AGT His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser 580 585 590	1774
GGT CAC CTC CAG GGT CAG CAT CCC TAC CTC ACA CCA TCC CCA GAG TCT Gly His Leu Gln Gly Gln His Pro Tyr Leu Thr Pro Ser Pro Glu Ser 595 600 605	1822
CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asn Trp Ser 610 615 620	1870
CAT CTC ACC ACC ACC CCT ACC CCT GCG GGT GCT GGA GGA GGT CAG CCG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Glu Arg 625 630 635	1918
GGA CCT GCG ACA CAC ATC TCT GAG CCA CCA CAC AAC AAC ATC CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGCAGAGTTC CACCTCCAGT GTAGAGACAT AACAGACITT TGTAAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTCG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAAG TGTTCCTATT CAGATAATGC AAGAGAAAGCA ATTGCTCAGT	2142
TTCACTCGGT ATCTGCAGAG CTTATTCATT ATTCTAATCT AATAAGACAA GTTGTGCGAA	2202
ATGCCAAGATC AATACAAAGCC TTGGGTCCAT GTTACTCTCT TTCTATTTCG AGAATAAGAT	2262
CGATGCTTAT TGAAGCCGAG ACATTCTTGC AGCTTGGACT GCATTTTAAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATCAGAA GATTCTACAC TAGCGTCTCT TTGGGAATTA TCCCTCGAA	2382
TTCTGCCGCA ATTGACCTAC GCATCTCTCT CTCCTTGGAC ATTCTTTTGT GTTCAATTCG	2442
TGCTTTTGGT TTTCACCTCT TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAGGAC	2502
CTTTGTGCTT TTGATCATTC TGGCCCATGA AAGCAACETT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCCGTA TCCCTTCGAG TCTCACAAGG TTTACTTTTC TATGGTTCTC AGCACAALAC	2622
TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACTCTA TTGTGTTCCT CTGCATATAT	2682
CATTCCTGCA CACAGAAAGG GAGAAAGATA CTTTCTTCA ACAAATTTTC CCGGCAGGAG	2742
ATCCCTTCAA CAGGCTGCAC CTTAATTTTT CTGTCTCTGT TCCAGGTCTT CATATAAACT	2802
TTACCAGGAA GAAGGGTGTG AGTTTGTGT TTTTCTGTGT ATGGGCTCTG TCACTCTAAA	2862
GTTTTATCCT TGATAGTCTA GTTACTATGA CCGTCCCCAC TTTTAAAAA CCAACAAAAAG	2922
GTTCGAATG TTGCAATGAC CAAGAGACAA GTTAACCTGT CCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CTTACTTCCT GCGAAGCATT CCAATGACTC CTTGTATGGA ACACATTTGT	3042
CCCAGATCTG AGCATTCCTG CCGTGTTCCT CTCACTTACC CACCATATGA AACATGCTT	3102
AACGTGTGAG CTTTTCCTT CATATCCACA GAAGAGACTG TCTCAAAATG TGTACCTTTC	3162

Figure 11 Cont'D

CCATTTAGCA CTGAACCTTC CTTAGCCCAA GCGACCCAGT GACAGTTC TCCTTTTGT	3222
CAGATGATCA GTCTCTACTC ATTATCTTGC TGCTTAAAGG CCCTCTCACC AATCTTTCTT	3282
TCACACCGTC TGGTCCGTGT TACTGCTATA CCCAGTATGT TCTCAGTCAA GACATGGACT	3342
TTATATGTTT AAGTGCACGA ATTGGAAGT TGGAGTCTT TCTATGATC CAAAACAGCC	3402
CTATAAGAAE GTTGCAAAAG GAGGAACAT ATAGCAGCCT TTGCTATTTT CTCTACCAT	3462
TTCTTTTCTT CTGAACCGGC CATGACATTC CCTTGGCAA CTAACTAGA AACTCAACAG	3522
AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG CACAACTATA GACTTGGTCA	3582
TGTTTCAGAC TGATTGCCCC TCACCTGAAT CCAGTCTCTG TATTCACTCT CTGGCAATT	3642
TCTTTCAGTT TCTTTTAAAG CCAGAACCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT	3702
CTTCTCTTTC TCGTTGGGGC AGTTAATAAT TGGTCCATGC CTACAGTCCA ACCTCCGTCC	3762
AGTCTCTTGA TGGCCATGAC ACCTGCCAAA TAAGTTCTGC CTGGCCATTT TGTAGATAAT	3822
AACAGGTCAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCTTT CTATCGCTGC	3882
AAGTATCCAT CAGTGCCTCC CACTTACCTG AATTGCTCTT CCGTGGCCCC ATATGGAAAC	3942
CGTCCGTCTC TGTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCTAT CCAATTTAT	4002
TGAACCAACA AAAATAATTA CTCTGCCCT CAGATAAGCA GATTAAATTT GTTCAATCTC	4062
TGCTTAAATC TCTCCATGTG CCAACATTCT CTCAGCCTCT TTCAATAGTGT CCAAACATTT	4122
TATCAATCTA AATGGTGAAT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGAGAG	4182
ACCTATCTGC ATGGACCCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTC	4242
GGGATGGCGA TCACTTTCTT CCCCTG	4268

Figure 12A

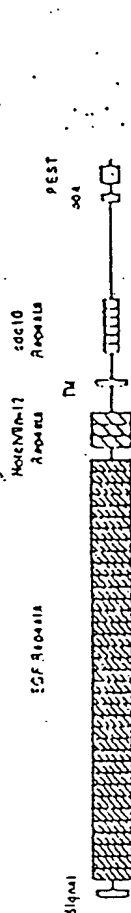


Figure 12A

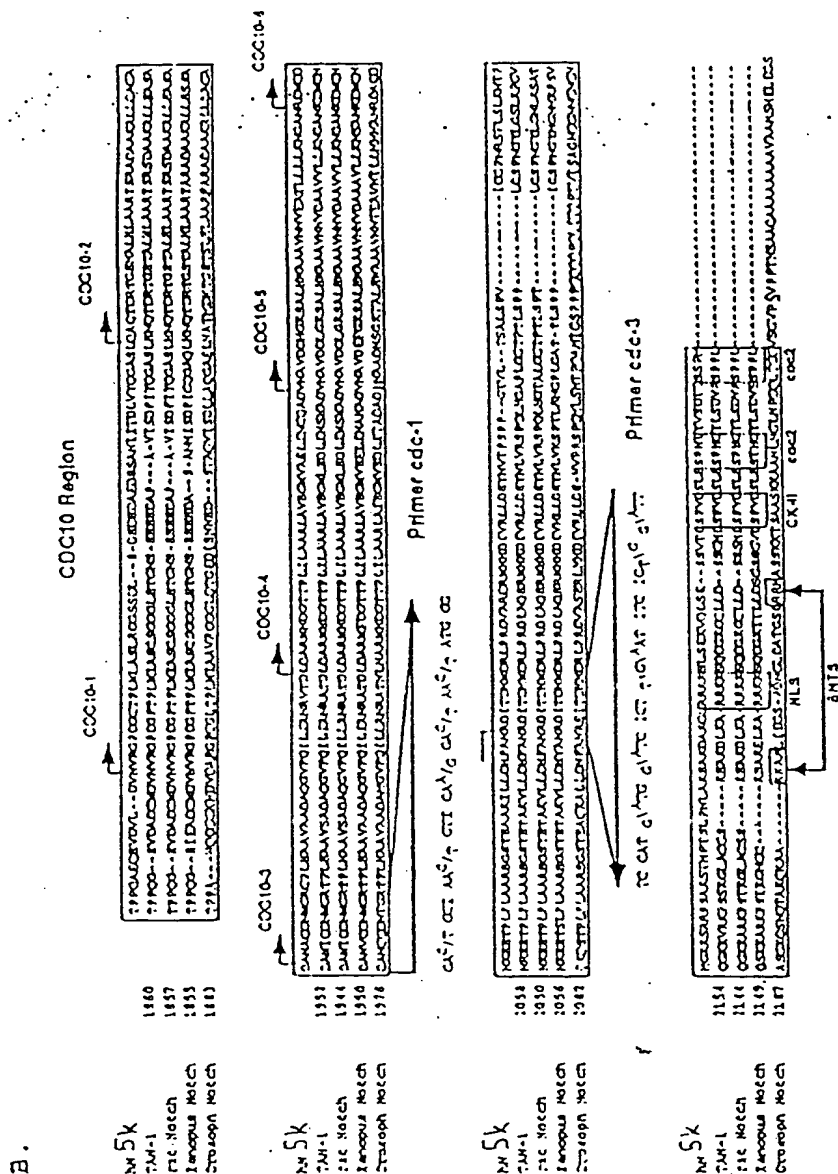


Figure 12B

[illegible]

Figure 12B Cont'D

PEST-containing Region

Figure 13

Potential signal cleavage site		EGF-like repeats	
Human	1	ALRAL LALLALMLC CA-----APA HA-----	33
TAN-1	1	PL LAPLALALL PA-----LAA RG-----	30
Xenopus	1	RIGLAVILCS LP-----VLT QG-----	29
Drosophila	1	INKNHVASL PASPLULLLT LAFANLPIV RCTOTALVA	117
Human	1	STSHPCFVS PCLNGCTCHM LSROT-YECT CQVGTQKEC QMTDGLSHP CANOSTCTTV --ANQFSNC LIGFTQKCE TDWNEC-DIP GHCHGCTCL	159
TAN-1	1	PLNAC-LTN PCRGCTCHL LST-LTEYKCR CPPOHAGSKC QANDPCASNP CANQZQCLPF --EATYCHC PEFHPTCR QNECCQKP RLCHGCTCH	136
Xenopus	1	PVNMAC-VNN PCRGCTCHL LST-LTEYKCR CPPOHAGSKC QANDPCASNP CANQZQCLPF --EATYCHC PEFHPTCR QNECCQKP RLCHGCTCH	159
Drosophila	1	AVPNAC-DHV TCLNGCTCOL KT-LEEVYCA CANOYTGERC ETNKLCAASP CRNGACTAL AGSSSTGSC PGTFTGDTCS YDIEEC-Q-S NPKYGGICV	233
Human	1	SLVPCASP CVNGCTCRQT GDTTECNCL PGTFTGDTCS NIDDCPNHRC QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	312
TAN-1	1	RPVPCSPSP CONQGTCTRT DQTSYCTCL PGTFTGDTCS NIDDCPNHRC QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	315
Xenopus	1	CLVNGCTCHL PGTFTGDTCS NIDDCPNHRC QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	314
Drosophila	1	CONAGICRSH G-LSYLCKCP KGFQGNKCE NYDGLCHLC QNGCTCTEDV DECLQPNH- CONQGTCAH	352
Human	1	AGLILCHLDA CTSNPKHGA LCTNPLAQ YICTCPQCYK QACTEDVDE CANANSNPE HAGVNTG	435
TAN-1	1	AGLILCHLDA CTSNPKHGA LCTNPLAQ YICTCPQCYK QACTEDVDE CANANSNPE HAGVNTG	434
Xenopus	1	AGLILCHLDA CTSNPKHGA LCTNPLAQ YICTCPQCYK QACTEDVDE CANANSNPE HAGVNTG	433
Drosophila	1	AGLILCHLDA CTSNPKHGA LCTNPLAQ YICTCPQCYK QACTEDVDE CANANSNPE HAGVNTG	476
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	552
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	554
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	553
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	596
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	577
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	573
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	572
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	710
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	736
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	732
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	731
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	735
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	914
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	911
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	909
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	943
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1034
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1031
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1029
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1069
Human	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1154
TAN-1	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1151
Xenopus	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1149
Drosophila	1	QNGOVGVGV VTYNCRCPPE WTCQFTCTEDV DECLQPNH- CONQGTCAH	1189

Figure 13 Cont'D

hum N	SNPCQICATC SDTIGYRCE CVPQYGVNC EYEDVOCNC PCQOCTCID LVNHKFCSP ROTGRLICEE NIDOCAR---	1267
TAN-1	PSPCQCATC TDYLOGYSCC CVAQYGVNC EYEDVOCNC PCQOCTCID LVNHKFCSP ROTGRLICEE NIDOCAR---	1271
Xen N	PNPCQCATC TDYLOGYSCC CVAQYGVNC EYEDVOCNC PCQOCTCID LVNHKFCSP ROTGRLICEE NIDOCAR---	1269
Dros N	SPQOQCATC RDLIGATCC CQOFGQOQC ELNIDOCAN PCQOCTCID LVNHKFCSP ROTGRLICEE NIDOCAR---	1300
hum H	CLSNPCSSIZ SLDCIQLTND YLVCRSATF GRHCETFDV CPHQCLNG TCVAASHPQ GFICRCPPGF SOARQCS---	1376
TAN-1	CLSNPCDARQ TQNCQVRND FHCRCBAGT GRHCETFDV CPHQCLNG TCVAASHPQ GFICRCPPGF SOARQCS---	1389
Xen H	CLSNPCDSRG TQNCIQLVND YHCRCBAGT GRHCETFDV CPHQCLNG TCVAASHPQ GFICRCPPGF SOARQCS---	1387
Dros N	CLSNPCSNAG TUDCVQLVND YHCRCBAGT GRHCETFDV CPHQCLNG TCVAASHPQ GFICRCPPGF SOARQCS---	1415
hum H	GC-ASSPCQ HGSCCHPQOQ PPTYSQCAP PFSGRCEI	1476
TAN-1	SPCLGQPCY NGTCCEPTE SPFYKCLCPA KNGLLCHL U DYSFG---	1501
Xen N	SPC-ASHPCY NGTCCEPTE SPFYKCLCPA KNGLLCHL U DYSFG---	1498
Dros H	DEC-SPNPCA QOACACEDLLG D--VECLCPS KMKGRCDY	1531
hum N	NN-QCELCN TVECLFDNFE CQNSKTKC -YDYKADHF KQNHQOCCN SEECGMDOLG CAQOPEL-L AEGTLVIVL	1591
TAN-1	SDCHGQOCCN SAGCLFDGFD CQNSKTKC -YDYKADHF KQNHQOCCN SEECGMDOLG CAQOPEL-L AEGTLVIVL	1519
Xen N	NOCKQOCCN MTGCLYDGF CQNSKTKC -YDYKADHF KQNHQOCCN SEECGMDOLG CAQOPEL-L AEGTLVIVL	1615
Dros N	KQNHQOCCN NAACHYDHD CEBKLSQCS LFDNYCQKH Y ODFCDYOCN NAECMDOLG CAQOPEL-L AEGTLVIVL	1650
hum N	YGEKSAHK QO--R-----	1680
TAN-1	YGOEEELK HPTRBAEOW APDALLQV KASLLPGQSE GGRRELOP HMDGSLVL EIDNRQOCCN SSOCTOSATO	1717
Xen N	YGOEEELK HPTRBAEOW APDALLQV KASLLPGQSE GGRRELOP HMDGSLVL EIDNRQOCCN SSOCTOSATO	1710
Dros H	WQNVREPEI EIDNRQOCCN SSOCTOSATO HMDGSLVL EIDNRQOCCN SSOCTOSATO HMDGSLVL EIDNRQOCCN	1745
hum N	CLAVAVIIL FILLQVTH KRKR--HOS LMLPEQFTLR ROASHKRE PUGQDVGXK NLSVOSEAN LGCTTSEH VDE-	1792
TAN-1	CLAVAVIIL FILLQVTH KRKR--HOS LMLPEQFTLR ROASHKRE PUGQDVGXK NLSVOSEAN LGCTTSEH VDE-	1817
Xen N	MLSHVLVL IIFVMMVIV NKRRREDS FGSPALQV PI-KRNGET PH-EDSVGLK PI-KRNGET PH-EDSVGLK	1831
Dros N	VITGIIILVII ALATFGVIL STQKRAHGV TWPFQFRAP AVHRSRRRD PHQOEHNLN KQVHOSQV QCPAH---	1861
hum N	PIDRRMTQO HLEAADRRT PSLATPPOA EQEVYDQV VNOPDOCTPL HIASLROGSS DLSEDEDAE	1902
TAN-1	QTDHROMTQO HLEAADRRT PSLATPPOA EQEVYDQV VNOPDOCTPL HIASLROGSS DLSEDEDAE	1934
Xen H	KTDPROMTQO HLEAADRRT PSLATPPOA EQEVYDQV VNOPDOCTPL HIASLROGSS DLSEDEDAE	1949
Dros H	EADQVHQA HLDVQV-R-ATH--TPP-A HQOQKHQV ADROPOLITPL HIAVRCOOL DTQEDENNE	1976
hum N	ANQDNHGR PLHAAVAAD QOVQILIRN RVTDLARH DDTPLILAA RLAVGQVAE LINCQDVNA	2022
TAN-1	ANQDNHGR PLHAAVAAD QOVQILIRN RVTDLARH DDTPLILAA RLAVGQVAE LINCQDVNA	2074
Xen N	ANQDNHGR PLHAAVAAD QOVQILIRN RVTDLARH DDTPLILAA RLAVGQVAE LINCQDVNA	2069
Dros N	ANQDNHGR PLHAAVAAD QOVQILIRN RVTDLARH DDTPLILAA RLAVGQVAE LINCQDVNA	2096
hum N	YDAKILLOH FANRITDTH DRLPVARD RHHIDVILL DYNVTPSP --OTVL--TS ALSPV-----	2127
TAN-1	YDAKILLOH FANRITDTH DRLPVARD RHHIDVILL DYNVTPSP --OTVL--TS ALSPV-----	2178
Xen H	YDAKILLOH FANRITDTH DRLPVARD RHHIDVILL DYNVTPSP --OTVL--TS ALSPV-----	2170
Dros N	YDAKILLOH FANRITDTH DRLPVARD RHHIDVILL DYNVTPSP --OTVL--TS ALSPV-----	2208
hum N	NLS	2169
TAN-1	GFPRKILSE KVOLSE--SS-VTLSPVBLE SPHTVSTT SSPK	2219
Xen N	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2213
Dros N	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2327
hum N	CK II	2169
TAN-1	GFPRKILSE KVOLSE--SS-VTLSPVBLE SPHTVSTT SSPK	2219
Xen H	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2213
Dros N	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2327
hum N	BNTS	2169
TAN-1	GFPRKILSE KVOLSE--SS-VTLSPVBLE SPHTVSTT SSPK	2219
Xen N	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2213
Dros N	A-PRKESOD KXCLLD--SS-OMLEPVBLE SPHTVSTT SSPK	2327

[illegible]

Figure 14

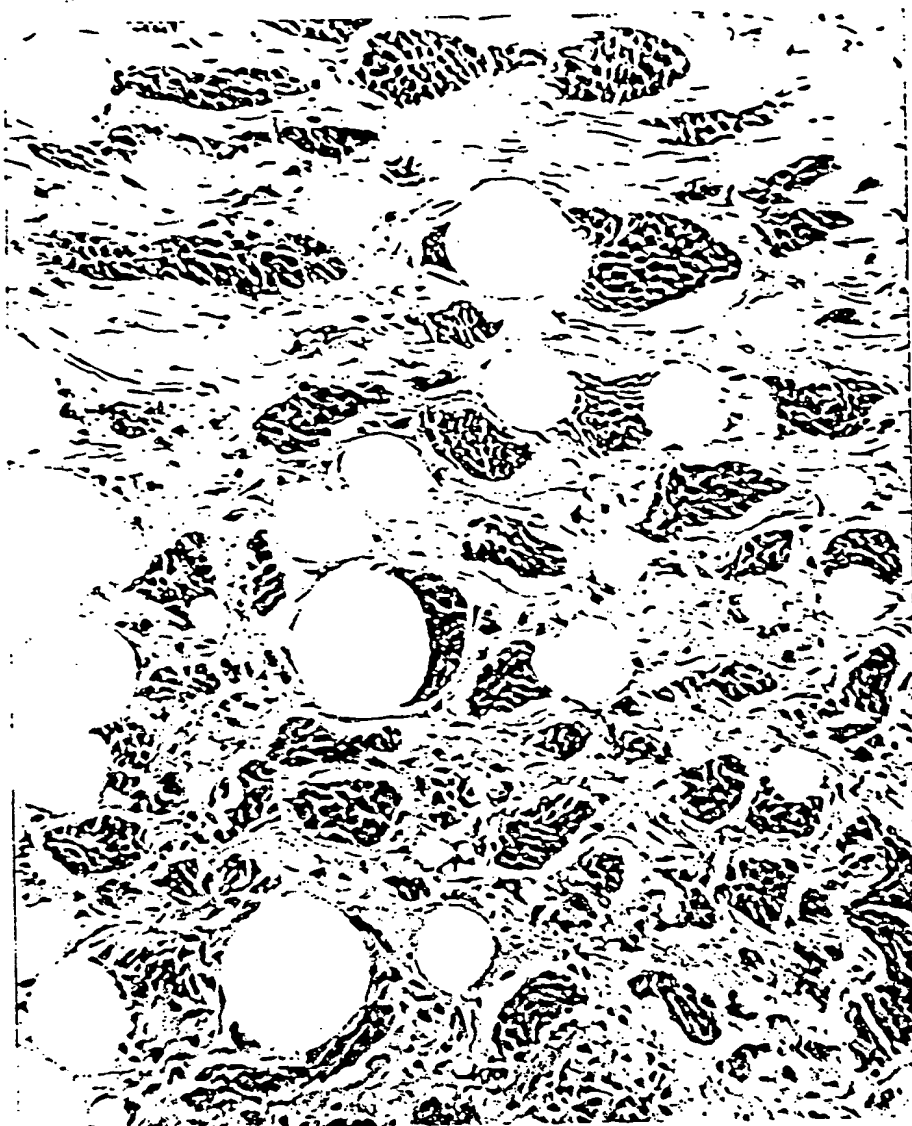


Figure 15A

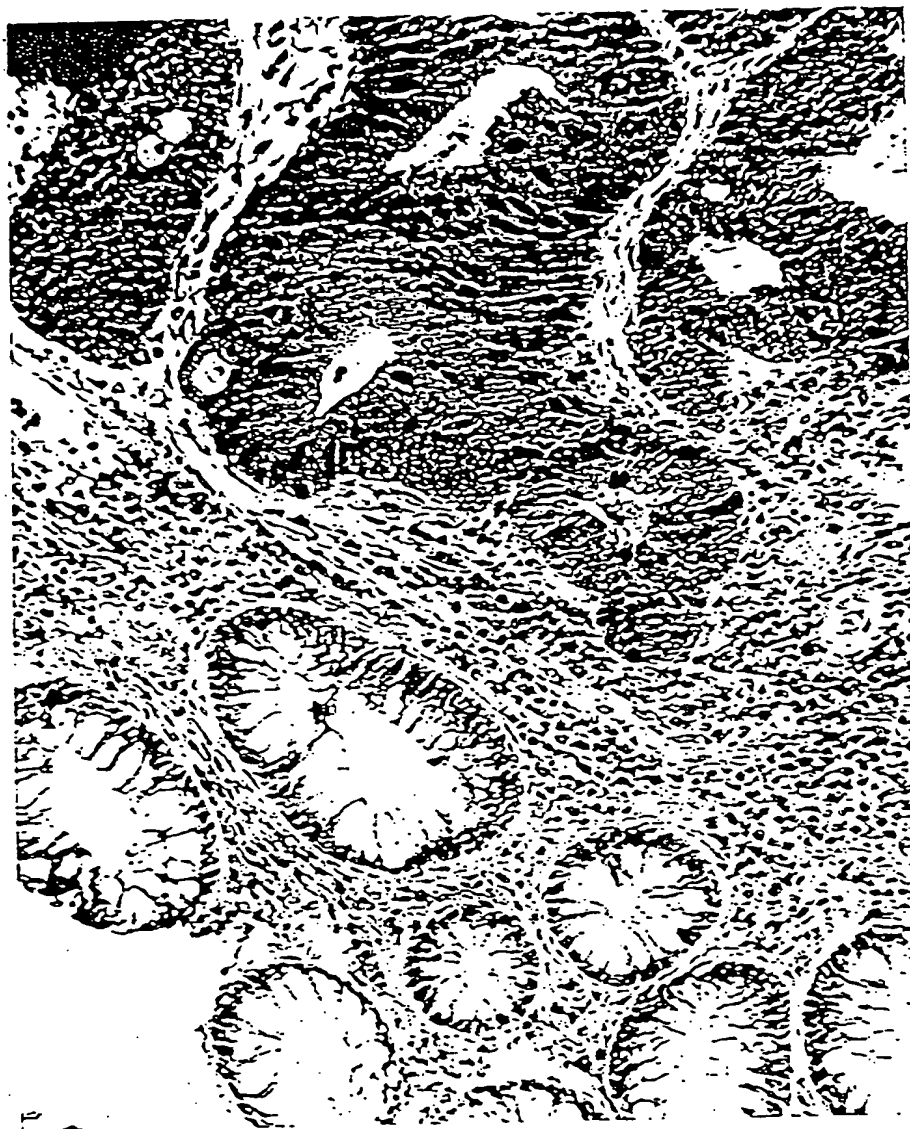


Figure 15B

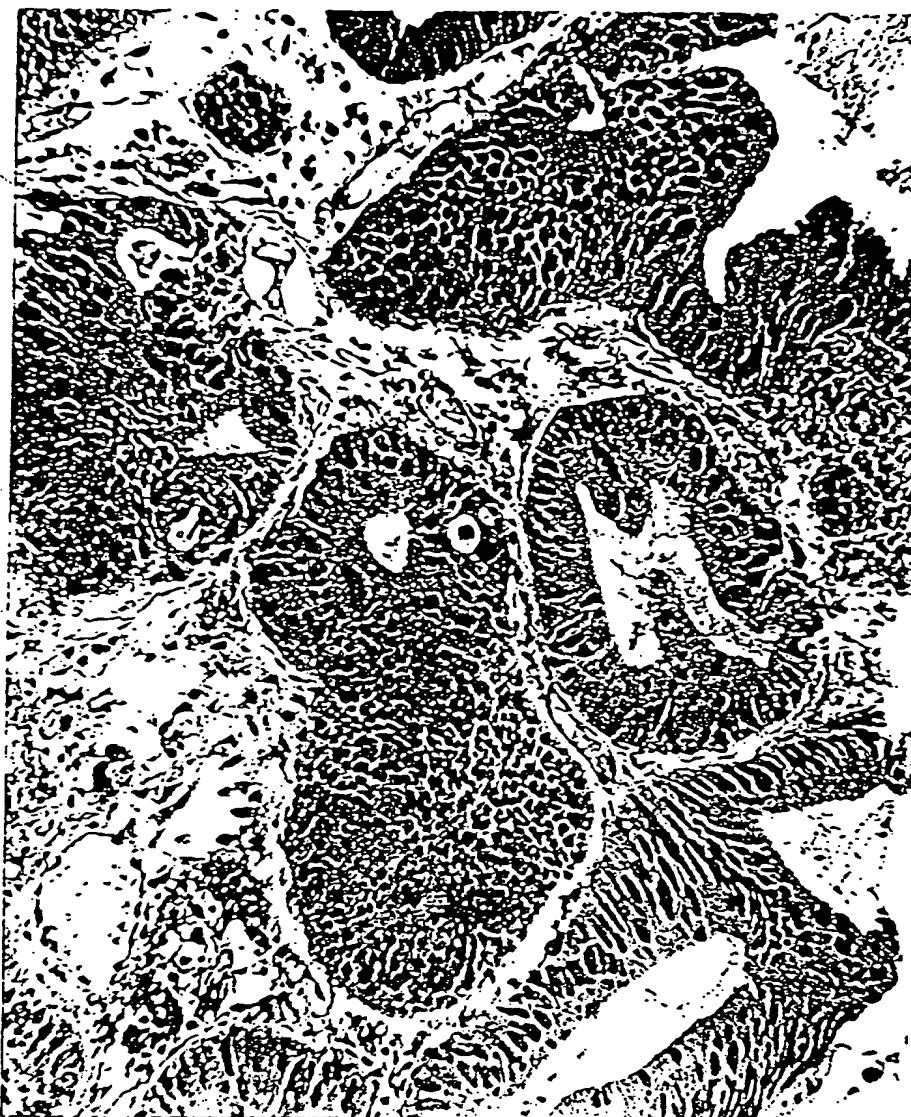


Figure 16A



Figure 16B



Figure 17

10 * CGGCCCTGG CCCGCTCTG CTGTGGGCG TCGTGGGCT CTGGCTGTC TCGCGGGCC CGCGCATGC ATTGCAGTG
 P A L R P A L L W A L L A L W L C C A A P A B A L Q C>
 100 * 110 * 120 * 130 * 140 * 150 * 160 * 170 * 180 *
 CGAGATGGCT ATGAACCTG TGTAAATGA GGAATGTG TTAACCTACCA CAATGCACA GGAFACTGCA AATGTCCAGA AGGTTCTTG
 R D G Y E P C V N E G M C V T Y H N G T G Y C K C P E G F L>
 190 * 200 * 210 * 220 * 230 * 240 * 250 * 260 * 270 *
 GGGGAATAT GTCAACATCG AGACCCCTGT GAGAAGAAC GCTGCCAGAA TGGTGGGACT TGTGTGGCC AGGCCATGCT GGGGAAGCC
 G E Y C Q H R D P C E K N R C Q N G G T C V A Q A M L G K A>
 280 * 290 * 300 * 310 * 320 * 330 * 340 * 350 * 360 *
 ACGTCCCGAT GTGCTCAGG GTTTACAGGA GAGACTGCC AGTACTCAAC ATCTCATCCA TGCTTGTGT CTGACCCCTG CCTGAATGGC
 T C R C A S G F T G E D C Q Y S T S H P C F V S R P C L N G>
 370 * 380 * 390 * 400 * 410 * 420 * 430 * 440 * 450 *
 GGCAATGCC ATATGCTCAG CCGGATACC TATAGTGA CCTGTCAAGT CCGGTTTACA GGTAAAGAGT GCCAATGAC GGATGCTGC
 G T C H M L S R D T Y E C T C Q V G F T G K E C Q W T D A C>
 460 * 470 * 480 * 490 * 500 * 510 * 520 * 530 * 540 *
 CTGTCTATC CCTGTGCAA TGAAGTACC TGTACCACTG TGGCCAACA GTTCTCTGC AATGCCCTCA CAGCTTCAC AGGGCAGAA
 L S H P C A N G S T C T T V A N Q F S C K C L T G F T G Q K>
 550 * 560 * 570 * 580 * 590 * 600 * 610 * 620 * 630 *
 TGTGACTG ATGTCAATG GTGTGACAT CCAGACACT GCCAGCATGG TGGACGCTG CTCACCTGC CTGTTCTTA CCAGTGCAG
 C E T D V N E C D I P G H C Q H G G T C L N L P G S Y Q C Q>
 640 * 650 * 660 * 670 * 680 * 690 * 700 * 710 * 720 *
 TGGCCCTCAGG GCTTCACAG CCAGTACTGT GACAGCTGT ATGTGCCCTG TGCACCTCA CCTTGTGTC ATGAGGCAC CTGTGGCAG
 C P Q G F T G Q Y C D S L Y V P C A P S P C V N G G T C R Q>
 730 * 740 * 750 * 760 * 770 * 780 * 790 * 800 * 810 *
 ACTGCTGACT TCACCTTGA GTGCACATGC CTTCCAGTT TTGAAGGAG CACCTGTGAG AGGAATATTG ATGACTGCC TACACACAGG
 T G D F T F E C N C L P G F E G S T C E R N I D D C P N H R>

Figure 17 Cont'D

820 * 830 * 840 * 850 * 860 * 870 * 880 * 890 * 900 *
 TGTCAAGATG GAGGGTTTG TGTGGATGGG GTCAACACIT ACACACTGGG CTGTCCGCCA CAATGACAG GACAGTTCTG CACAGAGAT
 C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D>

 910 * 920 * 930 * 940 * 950 * 960 * 970 * 980 * 990 *
 GTGATCAAT CCTGCTGCA GCGCAATGCC TGTCAAAATG GGGGACCTG TGGCAACCCG AATGAGGCT ATGGCTGTGT ATGTGTCAAC
 V D E C L L Q P N A C Q N G G T C A N R N G G Y G C V C V N>

 1000 * 1010 * 1020 * 1030 * 1040 * 1050 * 1060 * 1070 * 1080 *
 GGCTGGAGTG GAGATGACTG CAGTGAGAAC ATGTGATGTT GTGCTTCCG CTCTGTACT CCAGGCTCCA CCTGCATCGA CCGTGTGCC
 G W S G D D C S E N I D D C A F A S C T P G S T C I D R V A>

 1090 * 1100 * 1110 * 1120 * 1130 * 1140 * 1150 * 1160 * 1170 *
 TCCCTCTCTT GCATGTCCC AGAGGGGAG GCAGGTCTCC TGTGTCTCT TGTGTCTCT GATGATGCA TGCATGACGA ATCCTTGCCA CAGGGGGCA
 S F S C M C P E G K A G L L C H L D D A C I S N P C H K G A>

 1180 * 1190 * 1200 * 1210 * 1220 * 1230 * 1240 * 1250 * 1260 *
 CTGTGTGACA CCAACCCCT AATGGGCAA TATATTGCA CCTGCCACA AGCCTACAAA GGGGCTGACT GCACAGAAGA TGTGATGAA
 L C D T N P L N G Q Y I C T C P Q G Y K G A D C T E D V D E>

 1270 * 1280 * 1290 * 1300 * 1310 * 1320 * 1330 * 1340 * 1350 *
 TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGAA CACGGATGG GCCTTCCACT GTGAGTCTCT GAAGGTTAT
 C A M A N S N P C E H A G K C V N T D G A F H C E C L K G Y>

 1360 * 1370 * 1380 * 1390 * 1400 * 1410 * 1420 * 1430 * 1440 *
 GCAGGACCTC GTGTGAGAT GCACATCAAT GAGTCCCAT GAGTCCCAT CAGACCCCTG CCAGATGAT GCTACCTGTC TGGATAAGAT TGGAGCTTC
 A G P R C E M D I N E C H S D P C Q N D A T C L D K I G G F>

 1450 * 1460 * 1470 * 1480 * 1490 * 1500 * 1510 * 1520 * 1530 *
 ACATGCTGT GCATGCCAGG TTTCAAGGT GTGATTTG AATTAGAAAT AATGAATGT CAGAGCAACC CTTGTGTGAA CAATGGCAG
 T C L C M P G F K G V H C E L E I N E C Q S N P C V N N G Q>

 1540 * 1550 * 1560 * 1570 * 1580 * 1590 * 1600 * 1610 * 1620 *
 TGTGTGATA AATCAATCG TTTCCAGTC CTGTCTCTC CTGTTTCC TGGGCCAGTT TGGCAGATG ATATTGATGA CTGTTCCAGT
 C V D K V N R F Q C L C P P G F T G P V C Q I D I D C S S>

Figure 17 Cont'D

1630	1640	1650	1660	1670	1680	1690	1700	1710
ACTCCGTGTC	TGATGGGC	AAAGTGATC	GATCAGCGA	ATGCTATCA	ATGCCAGTT	ATCCAGTT	ATCCAGTT	ATCCAGTT
T P C	L N G A	K C I D	H P N G Y E	C Q C A T G	F T G V L C E			
1720	1730	1740	1750	1760	1770	1780	1790	1800
GAGACATTG	ACAACTGCA	CCCGATCCT	TGCCACCATG	GTCAGTGCA	GGATGTTAT	GATTCATCA	CCTGCATCG	CAATCCGGG
E N I	D N C D	P D P C	H G Q C Q D	G I D S Y T	C I C N P G			
1810	1820	1830	1840	1850	1860	1870	1880	1890
TACATGGCG	CCATCTGCG	TGACCAAGT	GATGAAGTT	ACAGCAGCC	TTGCCCTGAC	GATGTCGCT	GCATGACCT	GGTCAATGGC
Y M G	A I C S	D Q I D	E C Y S S P	C L N D	G R C I D L	V N G		
1900	1910	1920	1930	1940	1950	1960	1970	1980
TACCAGTGA	ACTGCCAGC	AGGCACGTCA	GGGTTAATT	GTGAATTAA	TTTGCATGAC	TGTGCAAGTA	ACCCTGTAT	CCATGATC
Y Q C	N C Q P	G T S G	V N C E I N	F D C A S N	P C I H G I			
1990	2000	2010	2020	2030	2040	2050	2060	2070
TGATGATG	GCATTAAATG	CTACAGTTGT	GTCTGCTAC	CAGATTAC	AGGCAGAGA	TGTAAATG	ACATTGATG	GTGTGCTCC
C M D	G I N R	Y S C V	C S P G F T	G Q R C N I	D I D E C A	S		
2080	2090	2100	2110	2120	2130	2140	2150	2160
AAATCCCTGTC	GCAAGGTGC	AAATGTATC	AACGGTGA	ATGGTTCCG	CTGTATATGC	CCCGAGGAC	CCCATCACCC	CACCTGCTAC
N P C	R K G A	T C I N	G V N G F R	C I C P E G	P H P S C Y			
2170	2180	2190	2200	2210	2220	2230	2240	2250
TACACAGTGA	ACGATGCTC	GAGCAATCC	TGCATCCATG	GAACGTGAC	TGGAGCTCTC	AGTGCATATA	ACTGTCTCTG	TGATCCAGGC
S Q V	N E C L	S N P C	I H G N C T	G G L S G Y	K C L C D A	G		
2260	2270	2280	2290	2300	2310	2320	2330	2340
TGGGTTGGCA	TCAACTGGA	AGTGACAAA	AATGAATGCC	TTTGCATCC	ATGCCAGAT	GGAGCACTT	GTGACATCT	GGTGAATGA
W V G	I N C E	V D K N	E C L S N P	C Q N G G T	C D N L V N	G		
2350	2360	2370	2380	2390	2400	2410	2420	2430
TACAGGTGA	CTTGAAGAA	GGGCTTAAA	GGCTATACT	GCAGGTGAA	TATTGATGA	TGTGCTCTCA	ATCCATGCT	GAACCAAGGA
Y R C	T C K F	G F K G	Y N C Q V N	I D E C A S	N P C L N Q	G		
2440	2450	2460	2470	2480	2490	2500	2510	2520

1	2530	2540	2550	2560	2570	2580	2590	2600	2610	*
2	ACCTGCTTTG	ATGACATAG	TGGCTACACT	TGCCACTGTS	TGCTGCCATA	CACAGGCAAG	AATTGTCAGA	CAGTATTGGC	TCCCTGTTCC	*
3	T C F	D D I S	G Y T	C H C	V L P Y	T G X	N C Q	T V L A	P C S	*
4	2530	2540	2550	2560	2570	2580	2590	2600	2610	*
5	CCAAACCCCT	GTGAGATGC	TGCTGTTGTC	AAAGAGTCAC	CAAAATTIGA	GAGTTATACT	TGCTTGTTG	CTCCTGGCTG	GCAAGGTCAG	*
6	P N P	C E N A	A V C	K E S	P N F E	S Y T	C L C	A P G W	Q G Q	*
7	2620	2630	2640	2650	2660	2670	2680	2690	2700	*
8	CGGTGTACCA	TTGACATTGA	CGAGTGTATC	TCCAAGCCCT	GCATGAACCA	TGGTCTTGCC	CATAACACCC	AGGGCAGCTA	CATGTGTCAA	*
9	R C T	I D I D	E C I	S K P	C M N H	G L C	H N T	Q G S Y	M C E	*
10	2710	2720	2730	2740	2750	2760	2770	2780	2790	*
11	ATGTCCACCAG	GCCTCAGTGS	TATGGACTGT	GAGCAGGACA	TTGATGACTG	CCCTGCCAAT	CCTTGCCAGA	ATGGAGGTTT	CTGTATGAGAT	*
12	C P P	G F S G	M D C	E E D	I D D C	L A N	P C Q	N G G S	C M D	*
13	2800	2810	2820	2830	2840	2850	2860	2870	2880	*
14	GGAGTGATA	CTTTCTCCTG	CCTCTGCTT	CCGGTTTCA	CTGGGATAA	GTGCCAGACA	GACATGAATG	AGTGTCTCAG	TGAACCCCTGT	*
15	G V N	T F S C	L C L	P G F	T G D K	C Q T	D M N	E C L S	E P C	*
16	2890	2900	2910	2920	2930	2940	2950	2960	2970	*
17	AAAGATGAG	GGACCTGCTC	TGACTAGCTC	AACAGTTACA	CTTGCAAGTG	CCAGGCAGGA	TTTGATGGAG	TCCATTGTGA	GAACAACATC	*
18	K N G	G T C S	D Y V	N S Y	T C K C	Q A G	F D G	V H C E	N N I	*
19	2980	2990	3000	3010	3020	3030	3040	3050	3060	*
20	AAACAGTACA	CTGACAGCTC	CTGTTTCAAT	GGTGACACAT	GGTTGATGG	GATTAACCTC	TTCTCTTGCT	TGTGCCCTGT	GGGTTTCACAT	*
21	N E C	T E S S	C F N	G G T	C V D G	I N S	F S C	L C P V	G F T	*
22	3070	3080	3090	3100	3110	3120	3130	3140	3150	*
23	GGATCCCTTCT	GCCTCCATGA	GATCAATGAA	TGCAGCTCTC	ATCCATGCTC	GAATGAGGGA	AGGTGTGTTG	ATGGCTGGG	TACCTACCGC	*
24	G S F	C L H E	I N E	C S S	H P C L	N E G	T C V	D G L G	T Y R	*
25	3160	3170	3180	3190	3200	3210	3220	3230	3240	*
26	TGCAGCTGCC	CCCTGGGCTA	CAGTGGGAAA	AACHTCTACA	COCTGGTENA	TCTCTGCACT	CGGTCTCCAT	GTAAAAACAA	AGGTACTTGT	*
27	C S C	P L G Y	T G K	N C Q	T L V N	L C S	R S P	C K N	K G T	*
28	3250	3260	3270	3280	3290	3300	3310	3320	3330	*

Figure 17 Cont'D

GTTCAGAAA AAGCAGAGTC CCAGTGCCTA TGTCCATCTG GATGGCTG TGCCTATTCT GACGTGCCCA ATGCTCTCTG TGACATAGCA
 V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>
 3340 3350 3360 3370 3380 3390 3400 3410 3420
 GCTCCAGGA GAGGTGCT TGTGAACAC TTGTGCCAGC ACTCAGTGT CTGCATCAAT GGTGGCAACA CCGATTACTG TCAGTCCCCC
 A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>
 3430 3440 3450 3460 3470 3480 3490 3500 3510
 CTGGGCTATA CTGGGAGCTA CTGTGAGCAG CAACTCGATG AGTGTGGTGC CAACCCCTGC CAGCAGGGGG CAACATGCCG TGACTTCATT
 L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>
 3520 3530 3540 3550 3560 3570 3580 3590 3600
 GGTGGATACA GATCGGAGTG TGTCCAGGC TATCAGGGTG TCAACTGCA GTATGAAGTG GATGAGTGC AGAATCAGCC CTGCCAGAAAT
 G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>
 3610 3620 3630 3640 3650 3660 3670 3680 3690
 GGAGGCACCT GTATTGACCT TGTGAACAT TTCAAGTGCT CTTCGCCACC AGGCACCTCG GCCCTACTCT GTGAAGAGAA CATTGATGAC
 G G T C I D L V N H F K C S C P P G T R G L L C E N I D D>
 3700 3710 3720 3730 3740 3750 3760 3770 3780
 TGTGCCGGG GTCCCATTTG CCTTAATGCT GGTCAATGCA TGAATAGAT TGAAGGCTAC AGTTGTGCT GCTTGCCTGG CTTTGTCTGG
 C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G>
 3790 3800 3810 3820 3830 3840 3850 3860 3870
 GAGCGTTGTG AGGGAGACAT CAACGAGTGC CTCTCCAAACC CCTGCAGCTC TGAGGGCAGC CTGGACTGTA TACAGCTCAC CAATGACTAC
 E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>
 3880 3890 3900 3910 3920 3930 3940 3950 3960
 CTGTGTGTTT GCCGTAGTGC CTTTACTGGC CGGCACCTGT AAACCTTCGT CGATGTGTGT CCGCAGATGC CCGCTCTGAA TGGAGGGACT
 L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>
 3970 3980 3990 4000 4010 4020 4030 4040 4050
 TGTGTGTGG CCAGTAACAT GCCTGATGGT TTCAATTGCC GTTGTCCCCC GGAATTTCC GGGCAAGGT GCCAGAGCAG CTGTGACAAA
 C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>
 4060 4070 4080 4090 4100 4110 4120 4130 4140
 GTGAATGTA GGAAGGGGGA GCAGTGTGTG CACACGGCCT CTGACCCCG CTGCTTCTGC CCCAGTCCCC GGAAGTCCGA GTACAGGTGT

Figure 17 Cont'D

V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G C>
 4150 4160 4170 4180 4190 4200 4210 4220 4230
 GCAGTAGCC CCTGCCAGCA CGGGGGCAGC TGCACCCCTC AGCGCAGCC TCCTATTAC TCCTGCCAGT GTGCCCCACC ATTCTGGGT
 A S S P C Q H G G S C B P Q R Q P P Y Y S C Q C A P P F S G>
 4240 4250 4260 4270 4280 4290 4300 4310 4320
 AGCGCTGT AACTCTAC GGCACCCCC AGCACCCCTC CTGCACCTG TCTGAGCCAG TATGTGCGG ACAAGCTCG GATGCGCTC
 S R C E L Y T A P P S T P P A T C L S Q Y C A D K A R D G V>
 4330 4340 4350 4360 4370 4380 4390 4400 4410
 TGTGATGAG CCTGCAACAG CCATGCCCTG CAGTGGATG GGGTGACTG TTCTCTCAC ATGAGAAC CCTGGGCCA CTGCTCTCC
 C D E A C N S H A C Q W D G G D C S L T M E N P W A N C S S>
 4420 4430 4440 4450 4460 4470 4480 4490 4500
 CCATTCCCT CTTGGGATTA TATCAACAC CAGTGTGATG AGCTGCA CAGGTGCGG TGCCTGTTG ACACTTTGA ATGCCAGGG
 P L P C W D Y I N N Q C D E L C N T V E C L F D N F E C Q G>
 4510 4520 4530 4540 4550 4560 4570 4580 4590
 AACAGCAAGA CATGCAAGTA TGACAATAC TGTGAGACC ACTTCAAGA CAACCACTGT AACGAGGGT GCAACACTGA GGAGTGTGT
 N S K T C K Y D K Y C A D H F K D N H C N Q G C N S E E C G>
 4600 4610 4620 4630 4640 4650 4660 4670 4680
 TGGATGGC TGGACTGTC TGTGACCAA CCTGAGAAC TGGCAGAGG TACCCTGTT ATTGTGTTT TGTGCCCACC TGAACAACCTG
 W D G L D C A A D Q P E N L A E G T L V I V V L M P P E Q L>
 4690 4700 4710 4720 4730 4740 4750 4760 4770
 CTCAGGATG CTCGAGCTT CTTCGGGCA CTGGGTACC TGTCCACAC CAACCTGCGC ATTAGCGGG ACTCCCAGG GGAATCATG
 L Q D A R S F L R A L G T L L H T N L R I K R D S Q G E L M>
 4780 4790 4800 4810 4820 4830 4840 4850 4860
 GTGTACCCCT ATTATGGTCA GAAGTCAGT GCTATGAAGA AACAGAGAT GACAGCAGA TCCCTTCCTG GTGAACAAGA ACAGGAGTG
 V Y P Y Y G E K S A A M K K Q R M T R R S L P G E Q E Q E V>
 4870 4880 4890 4900 4910 4920 4930 4940 4950
 GCGAGTATA AGTCTTCTT GGAATATGAC AACCGACAGT GTGTCAAGA CTCAGACAC TCTTCAAGA ACACGAGGC AGCAGCACT
 A G S K V F L R I D N R Q C V Q D S G H C F K M T D A A A A>

Figure 17 Cont'D

4960	4970	4980	4990	5000	5010	5020	5030	5040
CTCTGGCT	CTCAGGCA	ACAGGGACC	CTGTCTACC	CTCTTGTC	TGTCGTAGT	GAATCCCTGA	CTCCAGAACG	CACTCAGCTC
L L A S H A I Q G T L S Y P L V S V V S E S L T P E R T Q L>								
5050	5060	5070	5080	5090	5100	5110	5120	5130
CTCTATCC	TTGCTGTGC	TGTTGTATC	ATTCTGTTA	TTATCTGCT	GGGGTAATC	ATGCCAATC	GAAGCGTAA	GCATGCTCT
L Y L L A V A V V I I L F I I L L G V I M A K R K R K H G S>								
5140	5150	5160	5170	5180	5190	5200	5210	5220
CTCTGGCTC	CTGAAGTTT	CACTCTCCG	CGAGTCCAA	GCAATCAAA	GGTCTGTAG	CCAGTGGAC	AGCATGCTGT	GGGGTGA
L W L P E G F T L R R D A S N H K R R E P V G Q D A V G L K>								
5230	5240	5250	5260	5270	5280	5290	5300	5310
AATCTCTAG	TGCAAGTCTC	AGAGCTAAC	CTAATGGTA	CTGGAACAAG	TGAACACTGG	GTGATGATG	AAGGGCCCA	GCCAAAGAAA
N L S V Q V S E A N L I G T G T S E H W V D D E G P Q P K K>								
5320	5330	5340	5350	5360	5370	5380	5390	5400
GTAAGGCTG	AGATGAGGC	CTTACTCTCA	GAAGAGATG	ACCCATTGA	TGCAGGGCA	TGGACACAGC	AGCACTTGA	AGTGCAGAC
V K A E D E A L L S E E D D P I D R R P W T Q Q H L E A A D>								
5410	5420	5430	5440	5450	5460	5470	5480	5490
ATCCGTAGGA	CACCATCGCT	GGCTCTCACC	CTCTCTCAGG	CAGACAGGA	GGTGGATG	TTAGATGTA	ATGTCCGTGG	CCCAGATGGC
I R R T P S L A L T P P Q A E Q E V D V L D V N V R G P D G>								
5500	5510	5520	5530	5540	5550	5560	5570	5580
TGCACCCAT	TGATGTGGC	TTCTCTCGA	GGAGGCAGCT	CAGATTGAG	TGATGAAGAT	GAAGATCAG	AGCACTTTC	TGCTACATC
C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I>								
5590	5600	5610	5620	5630	5640	5650	5660	5670
ATCACAGACT	TGGTCTACCA	GGGTCCAGC	CTCCAGGCC	AGACAGACG	GACTGTGAG	ATGCCCTGC	ACCTGCAGC	CCGCTACTCA
I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S>								
5680	5690	5700	5710	5720	5730	5740	5750	5760
CGGCTGATG	CTGCCAAGC	TCTCTGGAT	GCAGGTGAG	ATGCCAATG	CCAGACAAC	ATGGCCCGCT	GTCCACTCCA	TGCTGCAGTG
R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V>								

Figure 17 Cont'D

5770	5780	5790	5800	5810	5820	5830	5840	5850
GCAGCTGATG	CCCAAGCTGT	CTTCCAGATT	CTGATTCGCA	ACCGAGTAAC	TGATCTAGAT	GCAGGATGA	ATGATGGTAC	TACACCCCTG
A A D A Q G V F Q I L I R N R V T D L D A R M N D G T T P L>								
5860	5870	5880	5890	5900	5910	5920	5930	5940
ATCTGGCTG	CCCGCTGGC	TGTGAGGGA	ATGTTGGAG	AACTATCAA	CTGCCAAGC	GATGTGATG	CAGTGGATGA	CCATGGAAA
I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K>								
5950	5960	5970	5980	5990	6000	6010	6020	6030
TCTGCTCTC	ACTGGGACG	TGCTGTCAAT	ANTGTGAGG	CAACTCTTT	GTTGTGAAA	ANTGGGGCA	ACCGAGACAT	GCAGGACAA
S A L H W A A A V N N V E A T L L L L K N G A N R D M Q D N>								
6040	6050	6060	6070	6080	6090	6100	6110	6120
AAGGAAGAGA	CACCTCTGTT	TTTGTGTCG	CGGAGGGGA	GCTATGAGC	AGCCAAGATC	CTGTGAGAC	ATTTGGCCAA	TGGAGACATC
K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I>								
6130	6140	6150	6160	6170	6180	6190	6200	6210
ACAGACCATA	TGATCGTCT	TCCCGGGAT	GTGGCTCGG	ATCCATGCA	CCATGACAT	GTGGCTTC	TGGATGAATA	CAATGTGACC
T D H M D R L P R D V A R D R M H H D I V R L L D E Y N V T>								
6220	6230	6240	6250	6260	6270	6280	6290	6300
CCAAGCCCTC	CAGGACCGT	GTTGACTCT	GCTCTCTAC	CTGTATCTG	TGGGCCCAAC	AGATCTTTC	TCAGCTGAA	GCACACCCA
P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P>								
6310	6320	6330	6340	6350	6360	6370	6380	6390
ATGGGCAAGA	AGCTAGACG	GGCAGTGCC	AAGAGTACCA	TGCTTACTAG	CCTCCCTAAC	CTTGCCAAGG	AGCCAAGGA	TGCCAAGGT
M G K K S R R P S A K S T M P T S L P N L A X E A K D A K G>								
6400	6410	6420	6430	6440	6450	6460	6470	6480
AGTAGGAGGA	AGAAGTCTCT	GAGTGAGAG	GTCCAAGTGT	CTGAGAGTTC	AGTAACTTTA	TCCCTGTG	ATTCCCTAGA	ATCTCTCAC
S R R K K S L S E K V Q L S E S S V T L S P V D S L E S P H>								
6490	6500	6510	6520	6530	6540	6550	6560	6570
ACGTATGTTT	CCGACACAC	ATCCTCTCCA	ATGATTACAT	CCCCTGGAT	CTTACAGGCC	TCACCCCAAC	CTATGTTGCC	CACCTGCCGC
T Y V S D T T S S P M I T S P G I L Q A S P N P M L A T A A>								
6580	6590	6600	6610	6620	6630	6640	6650	6660

Figure 17 Cont'D

CCCTCTGCC	CAGTCCATGC	CCAGCATGA	CTATCTTTT	CTAATCTCA	TGAATGCAG	CCTTTGGCAC	ATGGGGCCAG	CACCTGCTT	*
P P A	P V H A	Q H A	L S F	S N L H	E M O	P L A	H G A S	T V L>	*
6670	6680	6690	6700	6710	6720	6730	6740	6750	*
CCCTCAGTGA	GCAGTTGCT	ATCCACACAC	CACATTTGT	CTCCAGCAG	TGGCAGTCT	GGAGCTTCA	GTAGGCTCCA	TCCAGTCCA	*
P S V	S Q L L	S H H	H I V	S P G S	G S A	G S L	S R L H	P V P>	*
6760	6770	6780	6790	6800	6810	6820	6830	6840	*
GTCCACGAC	ATGGATGAA	CCGCATGGAG	GTGATGACA	CCAGTACAA	TGAGATGTT	GGTATGGTCC	TGGCTCCAGC	TGAGGGCACC	*
V P A	D W M N	R M E	V N E	T Q Y N	E M F	G M V	L A P A	E G T>	*
6850	6860	6870	6880	6890	6900	6910	6920	6930	*
CATCTGGCA	TAGCTCCCA	GAGCAGCCA	CCTGAAGGA	AGCACATAC	CACCCCTCG	GAGCCCTGC	CCCCATTTT	GACTTCCAG	*
H P G	I A P Q	S R P	P E G	K H I T	T P R	E P L	P P I V	T F Q>	*
6940	6950	6960	6970	6980	6990	7000	7010	7020	*
CTCATCCCTA	AAGCAGTAT	TGCCACACA	CGGGGGCTC	CCAGCCTCA	GTCCACCTGC	CCTCCAGCTG	TTGGGGGCC	CCTGCCACCC	*
L I P	K G S I	A Q P	A G A	P Q P Q	S T C	P P A	V A G P	L P T>	*
7030	7040	7050	7060	7070	7080	7090	7100	7110	*
ATGTACAGA	TTCAGAAAT	GGCCCGTTG	CCCAGTTGG	CTTCCCCAC	TGCCATGATG	CCCCAGCAG	ACGGCAGGT	AGCTCAGACC	*
M Y Q	I P E M	A R L	P S V	A F P T	A M M	P Q Q	D G Q V	A Q T>	*
7120	7130	7140	7150	7160	7170	7180	7190	7200	*
ATTCTCCAG	CCTATCATCC	TTTCCAGCC	TCTGTGGCA	AGTACCCAC	ACCCCTTCA	CAGCACAGTT	ATGCTTCTC	AAATGCTGCT	*
I L P	A Y H P	F P A	S V G	K Y P T	P P S	Q H S	Y A S S	N A A>	*
7210	7220	7230	7240	7250	7260	7270	7280	7290	*
GAGCGACAC	CCAGTCACAG	TGGTCACCTC	CAGGGTGAGC	ATCCCTACCT	GACACATCC	CCAGAGTCTC	CTGACCACTG	GTCAAGTTCA	*
E R T	P S H S	G H L	Q G E	H P Y L	T P S	P E S	P D Q W	S S S>	*
7300	7310	7320	7330	7340	7350	7360	7370	7380	*
TCACCCCACT	CTGCTTCTGA	CTGTACAGAT	GTGACACACA	GGCCTACCCC	TGGGGTCTG	GGAGGAGTTC	ACGGGGGACC	TGGGACACAC	*
S P B	S A S D	W S D	V T T	S P T P	G G A	G G G	Q R G P	G T H>	*
7390	7400	7410	7420	7430	7440	7450	7460	7470	*

	A	C	G	T	A	C	T	G	A	G	A	C	A	A		M	S	E	P	P	H	N	N	M	Q	V	Y	A		
ATGTCGAGC	CACCA	CACAA	CAATC	ACAG	GTTTAT	CCGT	GAGAC	AGTCC	ACCTCC	AGTG	TAGAC	ACATA	ACTGAC	TTTT	GTAAT	GCCTG														
7480	*		7490	*	7500	*	7510	*	7520	*	7530	*	7540	*	7550	*	7560													
CTGAGGAACA	AATGA	AGGTC	ATCCG	GGAGA	GAATG	AAGA	AATCT	CTGA	GCACG	CTCT	AGAGT	AGGA	AAGACA	AGAT	GTTCT	TATTC														
7570	*		7580	*	7590	*	7600	*	7610	*	7620	*	7630	*	7640	*	7650													
AGATAATCCA	AGAGNA	CAATTC	GCAGTT	TCAC	TGGGTA	TCTG	CAAGC	TTAT	TGATTA	TTCT	TAATTA	ATAAG	ACAAG	TTTGT	TGGAAA															
7660	*		7670	*	7680	*	7690	*	7700	*	7710	*	7720	*	7730	*	7740													
TGCAAGATGA	ATACA	AGCCT	TGGT	CCATG	TTTACT	CTCT	TCTAT	TGGA	GAATA	AGATG	GATG	CTTAT	TAT	GAAGC	CCAGA	CATCT	TGCA													
7750	*		7760	*	7770	*	7780	*	7790	*	7800	*	7810	*	7820	*	7830													
GCCTTGACTG	CATTT	TAAGC	CCTG	CAGGT	TCTG	CCATAT	CCATG	AGNAG	ATTCT	ACACT	ACGCT	CTGT	TGGGA	ATTAT	GCCT	TGGAAT														
7840	*		7850	*	7860	*	7870	*	7880	*	7890	*	7900	*	7910	*	7920													
TCTGCCCTGAA	TTGAC	CTAGG	CATCT	CCCTCC	TCC	TTGGACA	TTCT	TTTGT	CT	TTTCT	TGCT	TTTGGT	TGCA	CTCT	CCG	TGATTT														
7930	*		7940	*	7950	*	7960	*	7970	*	7980	*	7990	*	8000	*	8010													
AGCCCTACCA	GCATG	TATTA	GGG	CAAGACC	TTTGT	GCTTT	TGAT	CACTCT	GGCC	CAATGAA	AGCA	ACCTTG	GTC	CTCT	CTTC	CCCT	CTCTGTC													
8020	*		8030	*	8040	*	8050	*	8060	*	8070	*	8080	*	8090	*	8100													
TTCCCGGTAT	CCCTT	GAGT	CTCA	CAAGT	TTACT	TTTGT	ATG	GTCTCA	GCACA	ACCT	TTCA	AGTATG	TTG	TTCT	TTT	GGAA	ATGGA													
8110	*		8120	*	8130	*	8140	*	8150	*	8160	*	8170	*	8180	*	8190													
CATACTGTAT	TGTTG	TTCTC	TGCAT	ATATC	ATTCT	CTGAG	AGAGA	AGGGG	AGA	GAATAC	TTTCT	TCAA	CAAA	TTT	TGG	GGC	AGGAGA													
8200	*		8210	*	8220	*	8230	*	8240	*	8250	*	8260	*	8270	*	8280													
TCCCTCAAG	AGGCT	GCACC	TAA	TTTTTC	TTG	TCTGT	GT	GCAGG	CTCT	ATATA	AACTT	TAC	CAGGA	AG	AGGG	GTGTA	GTTT	GTGTT												
8290	*		8300	*	8310	*	8320	*	8330	*	8340	*	8350	*	8360	*	8370													
TTTCTGTGTA	TGGC	CTGT	CAGT	GTAAG	TTTT	TAT	CTCT	GAT	AGT	CTAG	TACT	ATAG	CC	TCCC	CACT	TTTT	TAAAC	CAGAAA	AGG											
8380	*		8390	*	8400	*																								

Figure 17 Cont'D

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8470	8480	8490	8500	8510	8520	8530	8540	8550
CATTGACTGC	CTGATATGGAA	CACATTTC	CCAGATCTGA	GCATTCTAGG	CCGTGTTTAC	TCACTCACCC	AGCATATGAA	ACTAGTCTTA
8560	8570	8580	8590	8600	8610	8620	8630	8640
ACTGTTGAGC	CTTTCCTTTC	ATATCCACAG	AAGACACTGT	CTCAATGTT	GTACCCCTTC	CANTTAGSAC	TGAACITTC	TTAGCCCAAG
8650	8660	8670	8680	8690	8700	8710	8720	8730
GGACCCAGTG	ACAGTTGCT	TCCGTTTGC	AGATGATCAG	TCTCTACTGA	TTAATCTTGT	GCTTAAGGC	CTGCTCACCA	ATCTTCTTT
8740	8750	8760	8770	8780	8790	8800	8810	8820
CACACCGTGT	GCTCCGNGTT	ACTGCTATAC	CCAGTATGTT	CTCAGTGAAG	ACATCGACTT	TATATGTTCA	AGTGCAGCAA	TTGCAAAAGTT
8830	8840	8850	8860	8870	8880	8890	8900	8910
GGACTTGT	TCTATGATCC	AAACAGCCC	TATAAGAAG	TTGGAAAGG	AGGAATATA	TAGCAGCCCT	TGCTATTTTC	TCCTACCAT
8920	8930	8940	8950	8960	8970	8980	8990	9000
TCCTTTTCTC	TGAAGCGGCC	ATGACATTCC	CTTTGGCAAC	TAACGTAGAA	ACTCAACAGA	ACATTTTCT	TTCCCTAGACT	CACCTTTTAG
9010	9020	9030	9040	9050	9060	9070	9080	9090
ATGATAATGG	ACAACTATAG	ACTTGCTCAT	TGTTCCAGACT	GATTCGCCCT	CACCTGATC	CACCTCTGT	ATTCTATGCTC	TTGGCAATTT
9100	9110	9120	9130	9140	9150	9160	9170	9180
CTTTGACTTT	CTTTTAAGG	CAGAGCAT	TTAGTTAAT	GTAGATAAAG	AATAGTTTC	TTCTCTTCT	CCTTGGGCCA	GTTAATTAAT
9190	9200	9210	9220	9230	9240	9250	9260	9270
GGTCCATGGC	TACACTGCCA	CTTCCGTCCA	GTGCTGTGAT	GCCCATGACA	CCTGCAGAAAT	AAGTTCTGCC	TGGGCATTTT	GTACATATTA
9280	9290	9300	9310	9320	9330	9340	9350	9360
ACAGGTGAAT	TCCCGACTCT	TTTGTTTGA	ATGACAGTTC	TCATTCCTTC	TATGGCTGCA	AGATGATCATC	AGTCTTCCC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
TTTGTCTGTC	GCTGGCCCCA	TATGGAACC	CTGGGTGCT	GTTGGCATAA	TAGTTTACAA	ATGGTTTTT	CAGTCTATC	CAAAATTAAT
9460	9470	9480	9490	9500	9510	9520	9530	9540

GAACCAACAA AAATATTAC TTCTGCCCTG AGATAAGCAG ATTAAGTTTG TTCAATTCTCT GCTTTATCT CTCCATGTGG CAACATTCTG *
9550 * 9560 * 9570 * 9580 * 9590 * 9600 * 9610 * 9620 * 9630 *
TCAGCCCTCTT TCATAGTGTG CAATCATTTT ATCATTCTAA ATGGTGACTC TCTGCCCTTG GACCCATTTA TTATTCAACAG ATGGGGAGAA *
9640 * 9650 * 9660 * 9670 * 9680 * 9690 * 9700 * 9710 * 9720 *
CCATATCTGCA TGGACCCCTCA CCATCTCTG TGCAGCACAC ACAGTCAGG GAGCCAGTGG CGATGGCGAT GACTTCTTC CCTGGGAAT *
TCC